

## SEQUENCE LISTING

<110> Genentech, Inc.  
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<120> Secreted and Transmembrane Polypeptides and Nucleic  
Acids Encoding the Same

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<140> 09/665,350  
<141> 2000-09-18

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<210> 2

<211> 353

<212> PRT

<213> Homo sapiens

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```

```

Arg Cys Arg Gly Leu Val Asp Lys Phe Asn Gln Gly Met Val Asp Thr
      35              40              45

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```

Ala Lys Lys Asn Phe Gly Gly Gly Asn Thr Ala Trp Glu Glu Lys Thr
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```

Leu Ser Lys Tyr Glu Ser Ser Glu Ile Arg Leu Leu Glu Ile Leu Glu
      65              70              75              80

```

```

Gly Leu Cys Glu Ser Ser Asp Phe Glu Cys Asn Gln Met Leu Glu Ala
      85              90              95

```

```

Gln Glu Glu His Leu Glu Ala Trp Trp Leu Gln Leu Lys Ser Glu Tyr
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```

```

Pro Asp Leu Phe Glu Trp Phe Cys Val Lys Thr Leu Lys Val Cys Cys
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Ser Pro Gly Thr Tyr Gly Pro Asp Cys Leu Ala Cys Gln Gly Gly Ser
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 Cys Thr Asp Cys Met Asp Gly Tyr Phe Ser Ser Leu Arg Asn Glu Thr  
 180 185 190  
 His Ser Ile Cys Thr Ala Cys Asp Glu Ser Cys Lys Thr Cys Ser Gly  
 195 200 205  
 Leu Thr Asn Arg Asp Cys Gly Glu Cys Glu Val Gly Trp Val Leu Asp  
 210 215 220  
 Glu Gly Ala Cys Val Asp Val Asp Glu Cys Ala Ala Glu Pro Pro Pro  
 225 230 235 240  
 Cys Ser Ala Ala Gln Phe Cys Lys Asn Ala Asn Gly Ser Tyr Thr Cys  
 245 250 255  
 Glu Glu Cys Asp Ser Ser Cys Val Gly Cys Thr Gly Glu Gly Pro Gly  
 260 265 270  
 Asn Cys Lys Glu Cys Ile Ser Gly Tyr Ala Arg Glu His Gly Gln Cys  
 275 280 285  
 Ala Asp Val Asp Glu Cys Ser Leu Ala Glu Lys Thr Cys Val Arg Lys  
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 Asn Glu Asn Cys Tyr Asn Thr Pro Gly Ser Tyr Val Cys Val Cys Pro  
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<211> 2206

<212> DNA

<213> Homo sapiens

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 aacagccctg gctgagggag ctgcagcgca gcagagtatc tgacggcgcc aggttgcgta 180  
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&lt;210&gt; 4

&lt;211&gt; 379

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 4

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Met Ala Arg Arg Ser Ala Phe Pro Ala Ala Ala Leu Trp Leu Trp Ser
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```

```

Ile Leu Leu Cys Leu Leu Ala Leu Arg Ala Glu Ala Gly Pro Pro Gln
                20                      25                      30

```

```

Glu Glu Ser Leu Tyr Leu Trp Ile Asp Ala His Gln Ala Arg Val Leu
        35                      40                      45

```

```

Ile Gly Phe Glu Glu Asp Ile Leu Ile Val Ser Glu Gly Lys Met Ala
        50                      55                      60

```

```

Pro Phe Thr His Asp Phe Arg Lys Ala Gln Gln Arg Met Pro Ala Ile

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		85		90		95
Ala Glu Tyr Phe Tyr Glu Phe Leu Ser Leu Arg Ser Leu Asp Lys Gly						
		100		105		110
Ile Met Ala Asp Pro Thr Val Asn Val Pro Leu Leu Gly Thr Val Pro						
		115		120		125
His Lys Ala Ser Val Val Gln Val Gly Phe Pro Cys Leu Gly Lys Gln						
		130		135		140
Asp Gly Val Ala Ala Phe Glu Val Asp Val Ile Val Met Asn Ser Glu						
		145		150		155
Gly Asn Thr Ile Leu Gln Thr Pro Gln Asn Ala Ile Phe Phe Lys Thr						
		165		170		175
Cys Gln Gln Ala Glu Cys Pro Gly Gly Cys Arg Asn Gly Gly Phe Cys						
		180		185		190
Asn Glu Arg Arg Ile Cys Glu Cys Pro Asp Gly Phe His Gly Pro His						
		195		200		205
Cys Glu Lys Ala Leu Cys Thr Pro Arg Cys Met Asn Gly Gly Leu Cys						
		210		215		220
Val Thr Pro Gly Phe Cys Ile Cys Pro Pro Gly Phe Tyr Gly Val Asn						
		225		230		235
Cys Asp Lys Ala Asn Cys Ser Thr Thr Cys Phe Asn Gly Gly Thr Cys						
		245		250		255
Phe Tyr Pro Gly Lys Cys Ile Cys Pro Pro Gly Leu Glu Gly Glu Gln						
		260		265		270
Cys Glu Ile Ser Lys Cys Pro Gln Pro Cys Arg Asn Gly Gly Lys Cys						
		275		280		285
Ile Gly Lys Ser Lys Cys Lys Cys Ser Lys Gly Tyr Gln Gly Asp Leu						
		290		295		300
Cys Ser Lys Pro Val Cys Glu Pro Gly Cys Gly Ala His Gly Thr Cys						
		305		310		315
His Glu Pro Asn Lys Cys Gln Cys Gln Glu Gly Trp His Gly Arg His						
		325		330		335
Cys Asn Lys Arg Tyr Glu Ala Ser Leu Ile His Ala Leu Arg Pro Ala						
		340		345		350

Gly Ala Gln Leu Arg Gln His Thr Pro Ser Leu Lys Lys Ala Glu Glu  
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 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
           oligonucleotide probe

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<210> 6  
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 <223> Description of Artificial Sequence: Synthetic  
           oligonucleotide probe

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<210> 7  
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 <223> Description of Artificial Sequence: Synthetic  
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<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 9  
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<210> 10  
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<220>  
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 oligonucleotide probe

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 <212> DNA  
 <213> Homo sapiens

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<210> 12

<211> 164

<212> PRT

<213> Homo sapiens

<400> 12

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```

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```

```

Pro Gly Leu His Leu Arg Gly Ile Arg Asp Ala Gly Gly Arg Tyr Cys
      35                      40                      45

```

```

Gln Glu Gln Asp Leu Cys Cys Arg Gly Arg Ala Asp Asp Cys Ala Leu
      50                      55                      60

```

```

Pro Tyr Leu Gly Ala Ile Cys Tyr Cys Asp Leu Phe Cys Asn Arg Thr
      65                      70                      75                      80

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```

Val Ser Asp Cys Cys Pro Asp Phe Trp Asp Phe Cys Leu Gly Val Pro
      85                      90                      95

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Pro Pro Phe Pro Pro Ile Gln Gly Cys Met His Gly Gly Arg Ile Tyr
      100                      105                      110

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Pro Val Leu Gly Thr Tyr Trp Asp Asn Cys Asn Arg Cys Thr Cys Gln
      115                      120                      125

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```

Glu Asn Arg Gln Trp His Gly Gly Ser Arg His Asp Gln Ser His Gln
      130                      135                      140

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Pro Gly Gln Leu Trp Leu Ala Gly Trp Glu Pro Gln Arg Leu Leu Gly
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His Asp Pro Gly

<210> 13  
 <211> 533  
 <212> DNA  
 <213> Homo sapiens

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 <222> (33)  
 <223> a, t, c or g

<220>  
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 <223> a, t, c or g

<220>  
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 <223> a, t, c or g

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 <223> a, t, c or g

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<210> 14  
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 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

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24

<210> 15

<211> 22

<212> DNA

<213> Artificial Sequence

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<210> 17

<211> 960

<212> DNA

<213> Homo sapiens

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<210> 18

<211> 189

<212> PRT

<213> Homo sapiens

&lt;400&gt; 18

Met Thr His Arg Thr Thr Thr Trp Ala Arg Arg Thr Ser Arg Ala Val  
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Thr Pro Thr Cys Ala Thr Pro Ala Gly Pro Met Pro Cys Ser Arg Leu  
 20 25 30

Pro Pro Ser Leu Arg Cys Ser Leu His Ser Ala Cys Cys Ser Gly Asp  
 35 40 45

Pro Ala Ser Tyr Arg Leu Trp Gly Ala Pro Leu Gln Pro Thr Leu Gly  
 50 55 60

Val Val Pro Gln Ala Ser Val Pro Leu Leu Thr Asp Leu Ala Gln Trp  
 65 70 75 80

Glu Pro Val Leu Val Pro Glu Ala His Pro Asn Ala Ser Leu Thr Met  
 85 90 95

Tyr Val Cys Thr Pro Val Pro His Pro Asp Pro Pro Met Ala Leu Ser  
 100 105 110

Arg Thr Pro Thr Arg Gln Ile Ser Ser Ser Asp Thr Asp Pro Pro Ala  
 115 120 125

Asp Gly Pro Ser Asn Pro Leu Cys Cys Cys Phe His Gly Pro Ala Phe  
 130 135 140

Ser Thr Leu Asn Pro Val Leu Arg His Leu Phe Pro Gln Glu Ala Phe  
 145 150 155 160

Pro Ala His Pro Ile Tyr Asp Leu Ser Gln Val Trp Ser Val Val Ser  
 165 170 175

Pro Ala Pro Ser Arg Gly Gln Ala Leu Arg Arg Ala Gln  
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&lt;210&gt; 19

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

&lt;400&gt; 19

tgctgtgcta ctctgcaaa gccc

24

&lt;210&gt; 20

&lt;211&gt; 24

&lt;212&gt; DNA



<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 20

tgcacaagtc ggtgtcacag cacg

24

<210> 21

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 21

agcaacgagg actgcctgca ggtggagaac tgcacccagc tggg

44

<210> 22

<211> 1200

<212> DNA

<213> Homo sapiens

<400> 22

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<210> 23

<211> 205

<212> PRT

<213> Homo sapiens

&lt;400&gt; 23

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Leu Ile Leu Cys Cys Gln Thr Gln Tyr Val Arg Asp Gln Gly Ala Met  
 20 25 30

Thr Asp Gln Leu Ser Arg Arg Gln Ile Arg Glu Tyr Gln Leu Tyr Ser  
 35 40 45

Arg Thr Ser Gly Lys His Val Gln Val Thr Gly Arg Arg Ile Ser Ala  
 50 55 60

Thr Ala Glu Asp Gly Asn Lys Phe Ala Lys Leu Ile Val Glu Thr Asp  
 65 70 75 80

Thr Phe Gly Ser Arg Val Arg Ile Lys Gly Ala Glu Ser Glu Lys Tyr  
 85 90 95

Ile Cys Met Asn Lys Arg Gly Lys Leu Ile Gly Lys Pro Ser Gly Lys  
 100 105 110

Ser Lys Asp Cys Val Phe Thr Glu Ile Val Leu Glu Asn Asn Tyr Thr  
 115 120 125

Ala Phe Gln Asn Ala Arg His Glu Gly Trp Phe Met Ala Phe Thr Arg  
 130 135 140

Gln Gly Arg Pro Arg Gln Ala Ser Arg Ser Arg Gln Asn Gln Arg Glu  
 145 150 155 160

Ala His Phe Ile Lys Arg Leu Tyr Gln Gly Gln Leu Pro Phe Pro Asn  
 165 170 175

His Ala Glu Lys Gln Lys Gln Phe Glu Phe Val Gly Ser Ala Pro Thr  
 180 185 190

Arg Arg Thr Lys Arg Thr Arg Arg Pro Gln Pro Leu Thr  
 195 200 205

&lt;210&gt; 24

&lt;211&gt; 28

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;120&gt;

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

&lt;400&gt; 24

cagtacgtga gggaccaggg cgccatga

28

&lt;110&gt; 25

<211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 25  
 ccggtgacct gcacgtgctt gccca 24

<210> 26  
 <211> 41  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<220>  
 <221> modified\_base  
 <222> (21)  
 <223> a, t, c or g

<400> 26  
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<210> 27  
 <211> 2479  
 <212> DNA  
 <213> Homo sapiens

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tctttgcttt ttaaactctt                                     2479

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&lt;210&gt; 28

&lt;211&gt; 660

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 28

```

Met Gly Leu Gln Thr Thr Lys Trp Pro Ser His Gly Ala Phe Phe Leu
  1                      5                      10                      15

```

```

Lys Ser Trp Leu Ile Ile Ser Leu Gly Leu Tyr Ser Gln Val Ser Lys
  20                      25                      30

```

```

Leu Leu Ala Cys Pro Ser Val Cys Arg Cys Asp Arg Asn Phe Val Tyr
  35                      40                      45

```

```

Cys Asn Glu Arg Ser Leu Thr Ser Val Pro Leu Gly Ile Pro Glu Gly
  50                      55                      60

```

```

Val Thr Val Leu Tyr Leu His Asn Asn Gln Ile Asn Asn Ala Gly Phe
  65                      70                      75                      80

```

```

Pro Ala Glu Leu His Asn Val Gln Ser Val His Thr Val Tyr Leu Tyr
  85                      90                      95

```

```

Gly Asn Gln Leu Asp Glu Phe Pro Met Asn Leu Pro Lys Asn Val Arg
  100                      105                      110

```

```

Val Leu His Leu Gln Glu Asn Asn Ile Gln Thr Ile Ser Arg Ala Ala
  115                      120                      125

```

Leu Ala Gln Leu Leu Lys Leu Glu Glu Leu His Leu Asp Asp Asn Ser  
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 Ile Ser Thr Val Gly Val Glu Asp Gly Ala Phe Arg Glu Ala Ile Ser  
 145 150 155 160  
 Leu Lys Leu Leu Phe Leu Ser Lys Asn His Leu Ser Ser Val Pro Val  
 165 170 175  
 Gly Leu Pro Val Asp Leu Gln Glu Leu Arg Val Asp Glu Asn Arg Ile  
 180 185 190  
 Ala Val Ile Ser Asp Met Ala Phe Gln Asn Leu Thr Ser Leu Glu Arg  
 195 200 205  
 Leu Ile Val Asp Gly Asn Leu Leu Thr Asn Lys Gly Ile Ala Glu Gly  
 210 215 220  
 Thr Phe Ser His Leu Thr Lys Leu Lys Glu Phe Ser Ile Val Arg Asn  
 225 230 235 240  
 Ser Leu Ser His Pro Pro Pro Asp Leu Pro Gly Thr His Leu Ile Arg  
 245 250 255  
 Leu Tyr Leu Gln Asp Asn Gln Ile Asn His Ile Pro Leu Thr Ala Phe  
 260 265 270  
 Ser Asn Leu Arg Lys Leu Glu Arg Leu Asp Ile Ser Asn Asn Gln Leu  
 275 280 285  
 Arg Met Leu Thr Gln Gly Val Phe Asp Asn Leu Ser Asn Leu Lys Gln  
 290 295 300  
 Leu Thr Ala Arg Asn Asn Pro Trp Phe Cys Asp Cys Ser Ile Lys Trp  
 305 310 315 320  
 Val Thr Glu Trp Leu Lys Tyr Ile Pro Ser Ser Leu Asn Val Arg Gly  
 325 330 335  
 Phe Met Cys Gln Gly Pro Glu Gln Val Arg Gly Met Ala Val Arg Glu  
 340 345 350  
 Leu Asn Met Asn Leu Leu Ser Cys Pro Thr Thr Thr Pro Gly Leu Pro  
 355 360 365  
 Leu Phe Thr Pro Ala Pro Ser Thr Ala Ser Pro Thr Thr Gln Pro Pro  
 370 375 380  
 Thr Leu Ser Ile Pro Asn Pro Ser Arg Ser Tyr Thr Pro Pro Thr Pro  
 385 390 395 400  
 Thr Thr Ser Lys Leu Pro Thr Ile Pro Asp Trp Asp Gly Arg Glu Arg

	405		410		415
Val Thr Pro Pro Ile Ser Glu Arg Ile Gln Leu Ser Ile His Phe Val	420		425		430
Asn Asp Thr Ser Ile Gln Val Ser Trp Leu Ser Leu Phe Thr Val Met	435		440		445
Ala Tyr Lys Leu Thr Trp Val Lys Met Gly His Ser Leu Val Gly Gly	450		455		460
Ile Val Gln Glu Arg Ile Val Ser Gly Glu Lys Gln His Leu Ser Leu	465		470		475
					480
Val Asn Leu Glu Pro Arg Ser Thr Tyr Arg Ile Cys Leu Val Pro Leu	485		490		495
Asp Ala Phe Asn Tyr Arg Ala Val Glu Asp Thr Ile Cys Ser Glu Ala	500		505		510
Thr Thr His Ala Ser Tyr Leu Asn Asn Gly Ser Asn Thr Ala Ser Ser	515		520		525
His Glu Gln Thr Thr Ser His Ser Met Gly Ser Pro Phe Leu Leu Ala	530		535		540
Gly Leu Ile Gly Gly Ala Val Ile Phe Val Leu Val Val Leu Leu Ser	545		550		555
					560
Val Phe Cys Trp His Met His Lys Lys Gly Arg Tyr Thr Ser Gln Lys	565		570		575
Trp Lys Tyr Asn Arg Gly Arg Arg Lys Asp Asp Tyr Cys Glu Ala Gly	580		585		590
Thr Lys Lys Asp Asn Ser Ile Leu Glu Met Thr Glu Thr Ser Phe Gln	595		600		605
Ile Val Ser Leu Asn Asn Asp Gln Leu Leu Lys Gly Asp Phe Arg Leu	610		615		620
Gln Pro Ile Tyr Thr Pro Asn Gly Gly Ile Asn Tyr Thr Asp Cys His	625		630		635
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Ile Pro Asn Asn Met Arg Tyr Cys Asn Ser Ser Val Pro Asp Leu Glu	645		650		655
His Cys His Thr	660				

<210> 29  
 <211> 21  
 <212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 29

eggtetacct gtatggcaac c

21

<210> 30

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 30

gcaggacaac cagataaacc ac

22

<210> 31

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 31

acgcagattt gagaaggctg tc

22

<210> 32

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 32

ttcacgggct gctcttgccc agctcttgaa gcttgaagag ctgcac

45

<210> 33

<211> 3449

<212> DNA

<213> Homo sapiens

<400> 33

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<210> 34

<211> 915

<212> PRT

<213> Homo sapiens

<400> 34

Met Glu Lys Met Leu Ala Gly Cys Phe Leu Leu Ile Leu Gly Gln Ile  
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Val Leu Leu Pro Ala Glu Ala Arg Glu Arg Ser Arg Gly Arg Ser Ile  
 20 25 30

Ser Arg Gly Arg His Ala Arg Thr His Pro Gln Thr Ala Leu Leu Glu  
 35 40 45

Ser Ser Cys Glu Asn Lys Arg Ala Asp Leu Val Phe Ile Ile Asp Ser  
 50 55 60

Ser Arg Ser Val Asn Thr His Asp Tyr Ala Lys Val Lys Glu Phe Ile  
 65 70 75 80

Val Asp Ile Leu Gln Phe Leu Asp Ile Gly Pro Asp Val Thr Arg Val  
 85 90 95

Gly Leu Leu Gln Tyr Gly Ser Thr Val Lys Asn Glu Phe Ser Leu Lys  
 100 105 110

Thr Phe Lys Arg Lys Ser Glu Val Glu Arg Ala Val Lys Arg Met Arg  
 115 120 125

His Leu Ser Thr Gly Thr Met Thr Gly Leu Ala Ile Gln Tyr Ala Leu  
 130 135 140

Asn Ile Ala Phe Ser Glu Ala Glu Gly Ala Arg Pro Leu Arg Glu Asn  
 145 150 155 160

Val Pro Arg Val Ile Met Ile Val Thr Asp Gly Arg Pro Gln Asp Ser  
 165 170 175

Val Ala Glu Val Ala Ala Lys Ala Arg Asp Thr Gly Ile Leu Ile Phe  
 180 185 190

Ala Ile Gly Val Gly Gln Val Asp Phe Asn Thr Leu Lys Ser Ile Gly  
 195 200 205

Ser Glu Pro His Glu Asp His Val Phe Leu Val Ala Asn Phe Ser Gln  
 210 215 220

Ile Glu Thr Leu Thr Ser Val Phe Gln Lys Lys Leu Cys Thr Ala His

225		230		235		240
Met Cys Ser Thr	Leu Glu His Asn Cys	Ala His Phe Cys	Ile Asn Ile			
	245		250		255	
Pro Gly Ser Tyr	Val Cys Arg Cys	Lys Gln Gly Tyr	Ile Leu Asn Ser			
	260		265		270	
Asp Gln Thr Thr	Cys Arg Ile Gln Asp	Leu Cys Ala Met	Glu Asp His			
	275		280		285	
Asn Cys Glu Gln	Leu Cys Val Asn	Val Pro Gly Ser	Phe Val Cys Gln			
	290		295		300	
Cys Tyr Ser Gly	Tyr Ala Leu Ala	Glu Asp Gly Lys	Arg Cys Val Ala			
	305		310		315	320
Val Asp Tyr Cys	Ala Ser Glu Asn	His Gly Cys Glu	His Glu Cys Val			
	325		330		335	
Asn Ala Asp Gly	Ser Tyr Leu Cys	Gln Cys His Glu	Gly Phe Ala Leu			
	340		345		350	
Asn Pro Asp Glu	Lys Thr Cys Thr	Arg Ile Asn Tyr	Cys Ala Leu Asn			
	355		360		365	
Lys Pro Gly Cys	Glu His Glu Cys	Val Asn Met Glu	Glu Ser Tyr Tyr			
	370		375		380	
Cys Arg Cys His	Arg Gly Tyr Thr	Leu Asp Pro Asn	Gly Lys Thr Cys			
	385		390		395	400
Ser Arg Val Asp	His Cys Ala Gln	Gln Asp His Gly	Cys Glu Gln Leu			
	405		410		415	
Cys Leu Asn Thr	Glu Asp Ser Phe	Val Cys Gln Cys	Ser Glu Gly Phe			
	420		425		430	
Leu Ile Asn Glu	Asp Leu Lys Thr	Cys Ser Arg Val	Asp Tyr Cys Leu			
	435		440		445	
Leu Ser Asp His	Gly Cys Glu Tyr	Ser Cys Val Asn	Met Asp Arg Ser			
	450		455		460	
Phe Ala Cys Gln	Cys Pro Glu Gly	His Val Leu Arg	Ser Asp Gly Lys			
	465		470		475	480
Thr Cys Ala Lys	Leu Asp Ser Cys	Ala Leu Gly Asp	His Gly Cys Glu			
	485		490		495	
His Ser Cys Val	Ser Ser Glu Asp	Ser Phe Val Cys	Gln Cys Phe Glu			
	500		505		510	

Gly Tyr Ile Leu Arg Glu Asp Gly Lys Thr Cys Arg Arg Lys Asp Val		
515	520	525
Cys Gln Ala Ile Asp His Gly Cys Glu His Ile Cys Val Asn Ser Asp		
530	535	540
Asp Ser Tyr Thr Cys Glu Cys Leu Glu Gly Phe Arg Leu Ala Glu Asp		
545	550	555 560
Gly Lys Arg Cys Arg Arg Lys Asp Val Cys Lys Ser Thr His His Gly		
	565 570	575
Cys Glu His Ile Cys Val Asn Asn Gly Asn Ser Tyr Ile Cys Lys Cys		
	580 585	590
Ser Glu Gly Phe Val Leu Ala Glu Asp Gly Arg Arg Cys Lys Lys Cys		
	595 600	605
Thr Glu Gly Pro Ile Asp Leu Val Phe Val Ile Asp Gly Ser Lys Ser		
	610 615	620
Leu Gly Glu Glu Asn Phe Glu Val Val Lys Gln Phe Val Thr Gly Ile		
625	630 635	640
Ile Asp Ser Leu Thr Ile Ser Pro Lys Ala Ala Arg Val Gly Leu Leu		
	645 650	655
Gln Tyr Ser Thr Gln Val His Thr Glu Phe Thr Leu Arg Asn Phe Asn		
	660 665	670
Ser Ala Lys Asp Met Lys Lys Ala Val Ala His Met Lys Tyr Met Gly		
	675 680	685
Lys Gly Ser Met Thr Gly Leu Ala Leu Lys His Met Phe Glu Arg Ser		
	690 695	700
Phe Thr Gln Gly Glu Gly Ala Arg Pro Leu Ser Thr Arg Val Pro Arg		
705	710 715	720
Ala Ala Ile Val Phe Thr Asp Gly Arg Ala Gln Asp Asp Val Ser Glu		
	725 730	735
Trp Ala Ser Lys Ala Lys Ala Asn Gly Ile Thr Met Tyr Ala Val Gly		
	740 745	750
Val Gly Lys Ala Ile Glu Glu Glu Leu Gln Glu Ile Ala Ser Glu Pro		
	755 760	765
Thr Asn Lys His Leu Phe Tyr Ala Glu Asp Phe Ser Thr Met Asp Glu		
	770 775	780
Ile Ser Glu Lys Leu Lys Lys Gly Ile Cys Glu Ala Leu Glu Asp Ser		
785	790 795	800



&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 37

gcctgtcagt gtcttgaggg acacgtgctc cgcagcgatg ggaag

45

&lt;210&gt; 38

&lt;211&gt; 1813

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 38

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cggcacctgc aggtccgtgc gtcccggggc tgggcgccct gactccgtcc cggccagggg 120
gggccatgat ttccctcccg gggcccttgg tgaccaactt gctgcggttt ttgttcttgg 180
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ggttgacagg ggtggaggga ggggaagtgg tgettccagc gtggtacacc ttgcacgggg 300
aggtgtcttc atcccagcca tgggaggtgc cctttgtgat gtggttcttc aaacagaaaag 360
aaaaggagga tcaggtgttg tctacatca atggggtcac aacaagcaaa cctggagtat 420
ccttgggtcta ctccatgccc tcccggaaac tgtccctgcg gctggagggt ctccaggaga 480
aagactctgg cccctacagc tgetccgtga atgtgcaaga caaacaaggc aaatctaggg 540
gccacagcat caaaacctta gaactcaatg tactggttcc tccagctcct ccatectgcc 600
gtctccaggg tgtgcccac gtgggggcaa acgtgacct gagctgccag tctccaagga 660
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ttgtatgaa aaa 1813

```

&lt;210&gt; 39

&lt;211&gt; 390

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 39

Met Ile Ser Leu Pro Gly Pro Leu Val Thr Asn Leu Leu Arg Phe Leu

1	5	10	15
Phe Leu Gly Leu Ser Ala Leu Ala Pro Pro Ser Arg Ala Gln Leu Gln	20	25	30
Leu His Leu Pro Ala Asn Arg Leu Gln Ala Val Glu Gly Gly Glu Val	35	40	45
Val Leu Pro Ala Trp Tyr Thr Leu His Gly Glu Val Ser Ser Ser Gln	50	55	60
Pro Trp Glu Val Pro Phe Val Met Trp Phe Phe Lys Gln Lys Glu Lys	65	70	75
Glu Asp Gln Val Leu Ser Tyr Ile Asn Gly Val Thr Thr Ser Lys Pro	85	90	95
Gly Val Ser Leu Val Tyr Ser Met Pro Ser Arg Asn Leu Ser Leu Arg	100	105	110
Leu Glu Gly Leu Gln Glu Lys Asp Ser Gly Pro Tyr Ser Cys Ser Val	115	120	125
Asn Val Gln Asp Lys Gln Gly Lys Ser Arg Gly His Ser Ile Lys Thr	130	135	140
Leu Glu Leu Asn Val Leu Val Pro Pro Ala Pro Pro Ser Cys Arg Leu	145	150	155
Gln Gly Val Pro His Val Gly Ala Asn Val Thr Leu Ser Cys Gln Ser	165	170	175
Pro Arg Ser Lys Pro Ala Val Gln Tyr Gln Trp Asp Arg Gln Leu Pro	180	185	190
Ser Phe Gln Thr Phe Phe Ala Pro Ala Leu Asp Val Ile Arg Gly Ser	195	200	205
Leu Ser Leu Thr Asn Leu Ser Ser Ser Met Ala Gly Val Tyr Val Cys	210	215	220
Lys Ala His Asn Glu Val Gly Thr Ala Gln Cys Asn Val Thr Leu Glu	225	230	235
Val Ser Thr Gly Pro Gly Ala Ala Val Val Ala Gly Ala Val Val Gly	245	250	255
Thr Leu Val Gly Leu Gly Leu Leu Ala Gly Leu Val Leu Leu Tyr His	260	265	270
Arg Arg Gly Lys Ala Leu Glu Glu Pro Ala Asn Asp Ile Lys Glu Asp	275	280	285

Ala Ile Ala Pro Arg Thr Leu Pro Trp Pro Lys Ser Ser Asp Thr Ile  
 290 295 300

Ser Lys Asn Gly Thr Leu Ser Ser Val Thr Ser Ala Arg Ala Leu Arg  
 305 310 315 320

Pro Pro His Gly Pro Pro Arg Pro Gly Ala Leu Thr Pro Thr Pro Ser  
 325 330 335

Leu Ser Ser Gln Ala Leu Pro Ser Pro Arg Leu Pro Thr Thr Asp Gly  
 340 345 350

Ala His Pro Gln Pro Ile Ser Pro Ile Pro Gly Gly Val Ser Ser Ser  
 355 360 365

Gly Leu Ser Arg Met Gly Ala Val Pro Val Met Val Pro Ala Gln Ser  
 370 375 380

Gln Ala Gly Ser Leu Val  
 385 390

<210> 40

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 40

agggctctcca ggagaaagac tc

22

<210> 41

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 41

attgtggggcc ttgcagacat agac

24

<210> 42

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 42  
 ggccacagca tcaaaacctt agaactcaat gtactgggtc ctccagctcc 50  
  
 <210> 43  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe  
  
 <400> 43  
 gtgtgacaca gcgtgggc 18  
  
 <210> 44  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe  
  
 <400> 44  
 gaccggcagg cttctgcg 18  
  
 <210> 45  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe  
  
 <400> 45  
 cagcagcttc agccaccagg agtgg 25  
  
 <210> 46  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe  
  
 <400> 46  
 ctgagccgtg ggctgcagtc tcgc 24  
  
 <210> 47



<211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 47

ccgactacga ctggttcttc atcatgcagg atgacacata tgtgc

45

<210> 48

<211> 2822

<212> DNA

<213> Homo sapiens

<400> 48

cgccaccact	gcggccaccg	ccaatgaaac	gcctcccgt	cctagtgggt	ttttccactt	60
tggtgaattg	ttcctatact	caaaattgca	ccaagacacc	ttgtctccca	aatgcaaaat	120
gtgaaatacg	caatggaatt	gaagcctgct	attgcaacat	gggattttca	ggaaatgggtg	180
tcacaatttg	tgaagatgat	aatgaatgtg	gaaatttaac	tcagtcctgt	ggcgaaaatg	240
ctaattgcac	taacacagaa	ggaagttatt	attgtatgtg	tgtacctggc	ttcagatcca	300
gcagtaacca	agacagggtt	atcactaatg	atggaaccgt	ctgtatagaa	aatgtgaatg	360
caaactgcca	tttagataat	gtctgtatag	ctgcaaatat	taataaaaact	ttaacaaaaa	420
tcagatccat	aaaagaacct	gtggctttgc	tacaagaagt	ctatagaaat	tctgtgacag	480
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taggttacaa	gaacaacact	atctcagcca	aggacacct	ttctaactca	actcttactg	600
aatttgtaaa	aaccgtgaat	aattttgttc	aaagggatac	atgtgtagtt	tgggacaagt	660
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ctttaaggat	atcccagagc	ttccaaaaga	ccacagagtt	tgatacaaat	tcaacggata	780
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atatggatgg	agactacata	aatatatttc	caaagagaaa	agctgcata	gattcaaatg	900
gcaatgttgc	agttgcattt	ttatattata	agagtattgg	tcctttgctt	tcacatctctg	960
acaacttctt	attgaaacct	caaaattatg	ataattctga	agaggaggaa	agagtcatat	1020
cttcagtaat	ttcagtcctca	atgagctcaa	accacccac	attatatgaa	cttgaaaaaa	1080
taacatttac	attaagtcac	cgaaaggtea	cagataggta	taggagtcta	tgtgcatttt	1140
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actcaaatga	gacccacacc	tcctgcccgt	gtaatcacct	gacacatttt	gcaattttga	1260
tgtcctctgg	tccttccatt	ggtattaaag	attataatat	tcttacaagg	atcactcaac	1320
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atgctttcca	ggggatgttc	atttttttat	tcctgtgtgt	tttatctaga	aagattcaag	2040
agaatatta	cagattgttc	aaaaatgtcc	cctgttggtt	tggatgttta	aggtaaacat	2100
agagaatggt	ggataattac	aactgcacaa	aaataaaaa	tccaagctgt	ggatgaccaa	2160

```

tgtataaaaa tgactcatca aattatccaa ttattaacta ctagacaaaa agtatttttaa 2220
atcagttttt ctgtttatgc tataggaact gtagataata aggtaaaatt atgtatcata 2280
tagatatact atgtttttct atgtgaaata gttctgtcaa aaatagtatt gcagatattt 2340
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gttgcccttg aaactagtcc cctaccacct cggtaatgag ctccattaca gaaagtggaa 2520
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acctccacaa attgaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2820
aa

```

&lt;210&gt; 49

&lt;211&gt; 690

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 49

```

Met Lys Arg Leu Pro Leu Leu Val Val Phe Ser Thr Leu Leu Asn Cys
  1              5              10              15

```

```

Ser Tyr Thr Gln Asn Cys Thr Lys Thr Pro Cys Leu Pro Asn Ala Lys
      20              25              30

```

```

Cys Glu Ile Arg Asn Gly Ile Glu Ala Cys Tyr Cys Asn Met Gly Phe
      35              40              45

```

```

Ser Gly Asn Gly Val Thr Ile Cys Glu Asp Asp Asn Glu Cys Gly Asn
      50              55              60

```

```

Leu Thr Gln Ser Cys Gly Glu Asn Ala Asn Cys Thr Asn Thr Glu Gly
      65              70              75              80

```

```

Ser Tyr Tyr Cys Met Cys Val Pro Gly Phe Arg Ser Ser Ser Asn Gln
      85              90              95

```

```

Asp Arg Phe Ile Thr Asn Asp Gly Thr Val Cys Ile Glu Asn Val Asn
      100              105              110

```

```

Ala Asn Cys His Leu Asp Asn Val Cys Ile Ala Ala Asn Ile Asn Lys
      115              120              125

```

```

Thr Leu Thr Lys Ile Arg Ser Ile Lys Glu Pro Val Ala Leu Leu Gln
      130              135              140

```

```

Glu Val Tyr Arg Asn Ser Val Thr Asp Leu Ser Pro Thr Asp Ile Ile
      145              150              155              160

```

```

Thr Tyr Ile Glu Ile Leu Ala Glu Ser Ser Ser Leu Leu Gly Tyr Lys
      165              170              175

```

```

Asn Asn Thr Ile Ser Ala Lys Asp Thr Leu Ser Asn Ser Thr Leu Thr

```

180					185					190					
Glu	Phe	Val	Lys	Thr	Val	Asn	Asn	Phe	Val	Gln	Arg	Asp	Thr	Phe	Val
		195					200					205			
Val	Trp	Asp	Lys	Leu	Ser	Val	Asn	His	Arg	Arg	Thr	His	Leu	Thr	Lys
	210						215					220			
Leu	Met	His	Thr	Val	Glu	Gln	Ala	Thr	Leu	Arg	Ile	Ser	Gln	Ser	Phe
	225						230					235			240
Gln	Lys	Thr	Thr	Glu	Phe	Asp	Thr	Asn	Ser	Thr	Asp	Ile	Ala	Leu	Lys
				245					250					255	
Val	Phe	Phe	Phe	Asp	Ser	Tyr	Asn	Met	Lys	His	Ile	His	Pro	His	Met
			260					265					270		
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Tyr	Asp	Ser	Asn	Gly	Asn	Val	Ala	Val	Ala	Phe	Leu	Tyr	Tyr	Lys	Ser
	290						295					300			
Ile	Gly	Pro	Leu	Leu	Ser	Ser	Ser	Asp	Asn	Phe	Leu	Leu	Lys	Pro	Gln
	305						310					315			320
Asn	Tyr	Asp	Asn	Ser	Glu	Glu	Glu	Glu	Arg	Val	Ile	Ser	Ser	Val	Ile
				325					330					335	
Ser	Val	Ser	Met	Ser	Ser	Asn	Pro	Pro	Thr	Leu	Tyr	Glu	Leu	Glu	Lys
			340					345					350		
Ile	Thr	Phe	Thr	Leu	Ser	His	Arg	Lys	Val	Thr	Asp	Arg	Tyr	Arg	Ser
		355					360					365			
Leu	Cys	Ala	Phe	Trp	Asn	Tyr	Ser	Pro	Asp	Thr	Met	Asn	Gly	Ser	Trp
	370						375					380			
Ser	Ser	Glu	Gly	Cys	Glu	Leu	Thr	Tyr	Ser	Asn	Glu	Thr	His	Thr	Ser
	385						390					395			400
Cys	Arg	Cys	Asn	His	Leu	Thr	His	Phe	Ala	Ile	Leu	Met	Ser	Ser	Gly
				405					410					415	
Pro	Ser	Ile	Gly	Ile	Lys	Asp	Tyr	Asn	Ile	Leu	Thr	Arg	Ile	Thr	Gln
			420					425					430		
Leu	Gly	Ile	Ile	Ile	Ser	Leu	Ile	Cys	Leu	Ala	Ile	Cys	Ile	Phe	Thr
		435					440					445			
Phe	Trp	Phe	Phe	Ser	Glu	Ile	Gln	Ser	Thr	Arg	Thr	Thr	Ile	His	Lys
	450						455					460			

[illegible]

<223> a, t, c or g

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 gtattgggtcc ctttgccttc atcatctgac aacttcttat tgaaacctca aaattatgat 180  
 aattctgaag aggaggaaag agtcatatct tcagtaattt cagtctcaat gagctcaaac 240  
 ccaccacat tatatgaact tgaaaaaata acatttacat taagtcacg aaaggtcaca 300  
 gataggtata ggagtctatg tggcattttg gaatactcac ctgataccat gaatggcagc 360  
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 aatcacctga cacattttgc aattttgatg tctctgggc cttccattgg tattaagat 480  
 tataatattc ttacaaggat cactcaacta ggaataatta ttctactgat ttgtcttgcc 540  
 atatgcattt ttacctctg gttcttcagt gaaattcaaa gcaccagga 589

<210> 51

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 51

ggtaatgagc tccattacag

20

<210> 52

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 52

ggagtagaaa gcgcatgg

18

<210> 53

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 53

cacctgatac catgaatggc ag

22

<210> 54

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 54

cgagctcgaa ttaattcg

18

<210> 55

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 55

ggatctcctg agctcagg

18

<210> 56

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 56

cctagttgag tgatccttgt aag

23

<210> 57

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 57

atgagaccca cacctcatgc cgctgtaatc acctgacaca ttttgcaatt

50

<210> 58

<211> 2137

<212> DNA

<213> Homo sapiens

<400> 58

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```

gggacaagaa gccgcgcgct gcctgcccgg gcccggggag ggggctgggg ctggggccgg 180
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tgctcggtg tcttgggcac ctaccggtg gcccgtaag gcgctactat ataaggctgc 300
cgccccggag ccgcgcgcgc gtcagagcag gaggcgtgcg tccaggatct agggccacga 360
ccatcccaac ccggcactca cagccccgca gccatcccgc gtcgcgcgcc agcctcccgc 420
acccccatcg ccggagctgc gccgagagcc ccagggaagt gccatgcgga gccgggtgtgt 480
ggtggtccac gtatggatcc tggccggcct ctggctggcc gtggccgggc gccccctcgc 540
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cctgtacacc tccggcccc acgggctctc cagctgcttc ctgcgcaccc gtgcgcacgg 660
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taaatttcac tcaaccccat gtgggaattg atctatatct ctacttccag ggaccatttg 1620
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gaaccctttc ccagcactt ggttttccaa catgatatt atgagtaatt tattttgata 2040
tgtacatctc ttattttctt acattattta tgccccaaa ttatatttat gtatgtaagt 2100
gaggtttgtt ttgtatatta aaatggagtt tgtttgt 2137

```

&lt;210&gt; 59

&lt;211&gt; 216

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 59

```

Met Arg Ser Gly Cys Val Val Val His Val Trp Ile Leu Ala Gly Leu
  1             5             10             15

```

```

Trp Leu Ala Val Ala Gly Arg Pro Leu Ala Phe Ser Asp Ala Gly Pro
          20          25          30

```

```

His Val His Tyr Gly Trp Gly Asp Pro Ile Arg Leu Arg His Leu Tyr
      35          40          45

```

```

Thr Ser Gly Pro His Gly Leu Ser Ser Cys Phe Leu Arg Ile Arg Ala
      50          55          60

```

Asp Gly Val Val Asp Cys Ala Arg Gly Gln Ser Ala His Ser Leu Leu  
 65 70 75 80

Glu Ile Lys Ala Val Ala Leu Arg Thr Val Ala Ile Lys Gly Val His  
 85 90 95

Ser Val Arg Tyr Leu Cys Met Gly Ala Asp Gly Lys Met Gln Gly Leu  
 100 105 110

Leu Gln Tyr Ser Glu Glu Asp Cys Ala Phe Glu Glu Glu Ile Arg Pro  
 115 120 125

Asp Gly Tyr Asn Val Tyr Arg Ser Glu Lys His Arg Leu Pro Val Ser  
 130 135 140

Leu Ser Ser Ala Lys Gln Arg Gln Leu Tyr Lys Asn Arg Gly Phe Leu  
 145 150 155 160

Pro Leu Ser His Phe Leu Pro Met Leu Pro Met Val Pro Glu Glu Pro  
 165 170 175

Glu Asp Leu Arg Gly His Leu Glu Ser Asp Met Phe Ser Ser Pro Leu  
 180 185 190

Glu Thr Asp Ser Met Asp Pro Phe Gly Leu Val Thr Gly Leu Glu Ala  
 195 200 205

Val Arg Ser Pro Ser Phe Glu Lys  
 210 215

<210> 60

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 60

atccgcccag atggtacaa tgtgta

26

<210> 61

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 61

gcctcccggg ctccctgagc agtgccaaac agcggcagtg ta

42



<210> 62  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 62  
 ccagtccggt gacaagccca aa 22

<210> 63  
 <211> 1295  
 <212> DNA  
 <213> Homo sapiens

<400> 63  
 cccagaagtt caagggcccc cggcctcctg cgctcctgcc gccgggaccc tcgacctcct 60  
 cagagcagcc ggctgccgcc ccgggaagat ggcgaggagg agccgccacc gctcctcct 120  
 gctgctgctg cgctacctgg tggtcgccct gggctatcat aaggcctatg ggttttctgc 180  
 cccaaaagac caacaagtag tcacagcagt agagtaccaa gaggcctatt tagcctgcaa 240  
 aacccccaaag aagactgttt cctccagatt agagtgggaag aaactgggtc ggagtgtctc 300  
 ctttgtctac tatcaacaga ctcttcaagg tgattttaaa aatcgagctg agatgataga 360  
 tttcaatatc cggatcaaaa atgtgacaag aagtgatgag gggaaatata gttgtgaagt 420  
 tagtgccccca tctgagcaag gccaaaacct ggaagaggat acagtcactc tgggaagtatt 480  
 agtggctcca gcagttccat catgtgaagt accctcttct gctctgagtg gaactgtggt 540  
 agagctacga tgtcaagaca aagaaggga tccagctcct gaatacacat ggtttaagga 600  
 tggcatcctg ttgctagaaa atcccagact tggctcccaa agcaccacaa gctcatacac 660  
 aatgaataca aaaactggaa ctctgcaatt taatactgtt tccaaactgg aactggaga 720  
 atattcctgt gaagcccgca attctgttgg atatcgagg tgtcctggga aacgaatgca 780  
 agtagatgat ctcaacataa gtggcatcat agcagccgta gtagttgtgg ccttagtgat 840  
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 ctccctccag aagagtaatt cttcatctaa agccacgaca atgagtgaat atgtgcagtg 960  
 gctcacgctt gtaatcccag cactttggaa ggccgaggcg ggccggtcac gaggtcagga 1020  
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 ctgggcatgg tggcatgtgc ctgcagttcc agctgcttgg gagacaggag aatcacttga 1140  
 acccgggagg cggaggttgc agtgagctga gatcacgcca ctgcagtcca gctgggta 1200  
 cagagcaaga ttccatctca aaaaataaaa taaataaata aataaatact ggtttttacc 1260  
 tgtagaattc ttacaataaa tatagcttga tattc 1295

<210> 64  
 <211> 312  
 <212> PRT  
 <213> Homo sapiens

<400> 64  
 Met Ala Arg Arg Ser Arg His Arg Leu Leu Leu Leu Leu Arg Tyr  
 1 5 10 15  
 Leu Val Val Ala Leu Gly Tyr His Lys Ala Tyr Gly Phe Ser Ala Pro  
 20 25 30

Lys Asp Gln Gln Val Val Thr Ala Val Glu Tyr Gln Glu Ala Ile Leu  
           35                          40                          45

Ala Cys Lys Thr Pro Lys Lys Thr Val Ser Ser Arg Leu Glu Trp Lys  
           50                          55                          60

Lys Leu Gly Arg Ser Val Ser Phe Val Tyr Tyr Gln Gln Thr Leu Gln  
           65                          70                          75                          80

Gly Asp Phe Lys Asn Arg Ala Glu Met Ile Asp Phe Asn Ile Arg Ile  
                           85                          90                          95

Lys Asn Val Thr Arg Ser Asp Ala Gly Lys Tyr Arg Cys Glu Val Ser  
                           100                          105                          110

Ala Pro Ser Glu Gln Gly Gln Asn Leu Glu Glu Asp Thr Val Thr Leu  
           115                          120                          125

Glu Val Leu Val Ala Pro Ala Val Pro Ser Cys Glu Val Pro Ser Ser  
           130                          135                          140

Ala Leu Ser Gly Thr Val Val Glu Leu Arg Cys Gln Asp Lys Glu Gly  
           145                          150                          155                          160

Asn Pro Ala Pro Glu Tyr Thr Trp Phe Lys Asp Gly Ile Arg Leu Leu  
                           165                          170                          175

Glu Asn Pro Arg Leu Gly Ser Gln Ser Thr Asn Ser Ser Tyr Thr Met  
                           180                          185                          190

Asn Thr Lys Thr Gly Thr Leu Gln Phe Asn Thr Val Ser Lys Leu Asp  
           195                          200                          205

Thr Gly Glu Tyr Ser Cys Glu Ala Arg Asn Ser Val Gly Tyr Arg Arg  
           210                          215                          220

Cys Pro Gly Lys Arg Met Gln Val Asp Asp Leu Asn Ile Ser Gly Ile  
           225                          230                          235                          240

Ile Ala Ala Val Val Val Val Ala Leu Val Ile Ser Val Cys Gly Leu  
                           245                          250                          255

Gly Val Cys Tyr Ala Gln Arg Lys Gly Tyr Phe Ser Lys Glu Thr Ser  
           260                          265                          270

Phe Gln Lys Ser Asn Ser Ser Ser Lys Ala Thr Thr Met Ser Glu Asn  
           275                          280                          285

Val Gln Trp Leu Thr Pro Val Ile Pro Ala Leu Trp Lys Ala Ala Ala  
           290                          295                          300

Gly Gly Ser Arg Gly Gln Glu Phe

305

310

<210> 65  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 65  
 atcgttgtga agttagtgcc cc 22

<210> 66  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 66  
 acctgcgata tccaacagaa ttg 23

<210> 67  
 <211> 48  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 67  
 ggaagaggat acagtcactc tggaagtatt agtggctcca gcagttcc 48

<210> 68  
 <211> 2539  
 <212> DNA  
 <213> Homo sapiens

<400> 68  
 gacatcggag gtgggctagc actgaaactg cttttcaaga cgaggaagag gaggagaaaag 60  
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 gcatcatgct gctattcctg caaatactga agaagcatgg gatttaaata ttttacttct 180  
 aaataaatga attactcaat ctcttatgac catctataca tactccacct tcaaaaagta 240  
 catcaatatt atatcattaa ggaaatagta accttctctt ctccaatatg catgacattt 300  
 ttggacaatg caattgtggc actggcactt atttcagtga agaaaaactt tgtggttcta 360  
 tggcattcat catttgacaa atgcaagcat ctcccttata aatcagctcc tattgaactt 420  
 actagcactg actgtggaat ccttaagggc ccattacatt tctgaagaag aaagctaaga 480  
 tgaaggacat gccactccga attcatgtgc tacttggcct agctatcact acactagtag 540

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aagctgtaga taaaaaagtg gattgtccac ggttatgtac gtgtgaaatc aggccttggg 500
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taactttccc agccagattg ccagctaaca cacagattct tctctacag actaacaata 720
ttgcaaaaat tgaatactcc acagactttc cagtaaacct tactggcctg gatttatctc 780
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taggtttacc aacaaatatg tctaaaaaac caccaaggaa acctactcca aaaatgaac 2639

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&lt;210&gt; 69

&lt;211&gt; 708

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 69

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Met Lys Asp Met Pro Leu Arg Ile His Val Leu Leu Gly Leu Ala Ile
 1             5             10             15

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Thr Thr Leu Val Gln Ala Val Asp Lys Lys Val Asp Cys Pro Arg Leu
      20             25             30

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Cys Thr Cys Glu Ile Arg Pro Trp Phe Thr Pro Arg Ser Ile Tyr Met
      35             40             45

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Glu Ala Ser Thr Val Asp Cys Asn Asp Leu Gly Leu Leu Thr Phe Pro
      50             55             60

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Ala Arg Leu Pro Ala Asn Thr Gln Ile Leu Leu Leu Gln Thr Asn Asn  
 65 70 75 80  
 Ile Ala Lys Ile Glu Tyr Ser Thr Asp Phe Pro Val Asn Leu Thr Gly  
 85 90 95  
 Leu Asp Leu Ser Gln Asn Asn Leu Ser Ser Val Thr Asn Ile Asn Val  
 100 105 110  
 Lys Lys Met Pro Gln Leu Leu Ser Val Tyr Leu Glu Glu Asn Lys Leu  
 115 120 125  
 Thr Glu Leu Pro Glu Lys Cys Leu Ser Glu Leu Ser Asn Leu Gln Glu  
 130 135 140  
 Leu Tyr Ile Asn His Asn Leu Leu Ser Thr Ile Ser Pro Gly Ala Phe  
 145 150 155 160  
 Ile Gly Leu His Asn Leu Leu Arg Leu His Leu Asn Ser Asn Arg Leu  
 165 170 175  
 Gln Met Ile Asn Ser Lys Trp Phe Asp Ala Leu Pro Asn Leu Glu Ile  
 180 185 190  
 Leu Met Ile Gly Glu Asn Pro Ile Ile Arg Ile Lys Asp Met Asn Phe  
 195 200 205  
 Lys Pro Leu Ile Asn Leu Arg Ser Leu Val Ile Ala Gly Ile Asn Leu  
 210 215 220  
 Thr Glu Ile Pro Asp Asn Ala Leu Val Gly Leu Glu Asn Leu Glu Ser  
 225 230 235 240  
 Ile Ser Phe Tyr Asp Asn Arg Leu Ile Lys Val Pro His Val Ala Leu  
 245 250 255  
 Gln Lys Val Val Asn Leu Lys Phe Leu Asp Leu Asn Lys Asn Pro Ile  
 260 265 270  
 Asn Arg Ile Arg Arg Gly Asp Phe Ser Asn Met Leu His Leu Lys Glu  
 275 280 285  
 Leu Gly Ile Asn Asn Met Pro Glu Leu Ile Ser Ile Asp Ser Leu Ala  
 290 295 300  
 Val Asp Asn Leu Pro Asp Leu Arg Lys Ile Glu Ala Thr Asn Asn Pro  
 305 310 315 320  
 Arg Leu Ser Tyr Ile His Pro Asn Ala Phe Phe Arg Leu Pro Lys Leu  
 325 330 335  
 Glu Ser Leu Met Leu Asn Ser Asn Ala Leu Ser Ala Leu Tyr His Gly

340	345	350
Thr Ile Glu Ser Leu Pro Asn Leu Lys Glu Ile Ser Ile His Ser Asn		
355	360	365
Pro Ile Arg Cys Asp Cys Val Ile Arg Trp Met Asn Met Asn Lys Thr		
370	375	380
Asn Ile Arg Phe Met Glu Pro Asp Ser Leu Phe Cys Val Asp Pro Pro		
385	390	395 400
Glu Phe Gln Gly Gln Asn Val Arg Gln Val His Phe Arg Asp Met Met		
	405	410 415
Glu Ile Cys Leu Pro Leu Ile Ala Pro Glu Ser Phe Pro Ser Asn Leu		
	420	425 430
Asn Val Glu Ala Gly Ser Tyr Val Ser Phe His Cys Arg Ala Thr Ala		
	435	440 445
Glu Pro Gln Pro Glu Ile Tyr Trp Ile Thr Pro Ser Gly Gln Lys Leu		
	450	455 460
Leu Pro Asn Thr Leu Thr Asp Lys Phe Tyr Val His Ser Glu Gly Thr		
	465	470 475 480
Leu Asp Ile Asn Gly Val Thr Pro Lys Glu Gly Gly Leu Tyr Thr Cys		
	485	490 495
Ile Ala Thr Asn Leu Val Gly Ala Asp Leu Lys Ser Val Met Ile Lys		
	500	505 510
Val Asp Gly Ser Phe Pro Gln Asp Asn Asn Gly Ser Leu Asn Ile Lys		
	515	520 525
Ile Arg Asp Ile Gln Ala Asn Ser Val Leu Val Ser Trp Lys Ala Ser		
	530	535 540
Ser Lys Ile Leu Lys Ser Ser Val Lys Trp Thr Ala Phe Val Lys Thr		
	545	550 555 560
Glu Asn Ser His Ala Ala Gln Ser Ala Arg Ile Pro Ser Asp Val Lys		
	565	570 575
Val Tyr Asn Leu Thr His Leu Asn Pro Ser Thr Glu Tyr Lys Ile Cys		
	580	585 590
Ile Asp Ile Pro Thr Ile Tyr Gln Lys Asn Arg Lys Lys Cys Val Asn		
	595	600 605
Val Thr Thr Lys Gly Leu His Pro Asp Gln Lys Glu Tyr Glu Lys Asn		
	610	615 620

Asn Thr Thr Thr Leu Met Ala Cys Leu Gly Gly Leu Leu Gly Ile Ile  
625 630 635 640

Gly Val Ile Cys Leu Ile Ser Cys Leu Ser Pro Glu Met Asn Cys Asp  
645 650 655

Gly Gly His Ser Tyr Val Arg Asn Tyr Leu Gln Lys Pro Thr Phe Ala  
660 665 670

Leu Gly Glu Leu Tyr Pro Pro Leu Ile Asn Leu Trp Glu Ala Gly Lys  
675 680 685

Glu Lys Ser Thr Ser Leu Lys Val Lys Ala Thr Val Ile Gly Leu Pro  
690 695 700

Thr Asn Met Ser  
705

<210> 70  
<211> 1305  
<212> DNA  
<213> Homo sapiens

<400> 70  
gcccgggact ggcgcaaggt gccaagcaa ggaaagaaat aatgaagaga cacatgtgtt 60  
agctgcagcc ttttgaaaca cgcaagaagg aaatcaatag tgtggacagg gctggaacct 120  
ttaccacgct tgttgagta gatgaggaat gggctcgtga ttatgctgac attccagcat 180  
gaatctggtg gacctgtggt taaccctgtc cctctccatg tgtctcctcc tacaaagttt 240  
tggtctttatg atactgtgct ttcattctgc cagtatgtgt cccaagggct gtctttgttc 300  
ttcctctggg ggtttaaatg tcacctgtag caatgcaaat ctcaaggaaa tacctagaga 360  
tcttctctct gaaacagtct tactgtatct ggaactccat cagatcacat ctattcccaa 420  
tgaaattttt aaggacctcc atcaactgag agttctcaac ctgtccaaaa atggcattga 480  
gtttatcgat gagcatgcct tcaaaggagt agctgaaacc ttgcagactc tggacttgct 540  
cgacaatcgg attcaaagtg tgcacaaaaa tgccttcaat aacctgaagg ccagggccag 600  
aattgccaac aacctctggc actgcgactg tactctacag caagttctga ggagcatggc 660  
gtccaatcat gagacagccc acaactgat ctgtaaaacg tccgtgttgg atgaacatgc 720  
tggcagacca ttctcaatg ctgccaacga cgctgacctt tgtaacctcc ctaaaaaaac 780  
taccgattat gccatgctgg tcaccatggt tggtctgttc actatggtga tctcatatgt 840  
ggtatattat gtgaggcaaa atcaggagga tgcccggaga cacctcgaat acttgaaatc 900  
cctgccaaagc aggcagaaga aagcagatga acctgatgat attagcactg tggatatgtg 960  
tccaaactga ctgtcattga gaaagaaaga aagtagtttg cgattgcagt agaaataagt 1020  
ggtttacttc tcccatccat tgtaaacatt tgaaactttg tatttcagtt ttttttgaat 1080  
tatgccactg ctgaactttt acaaacact acaacataaa taatttgagt ttaggtgatc 1140  
cacccttaa ttgtacccc gatggtatat ttctgagtaa gctactatct gaacattagt 1200  
tagatccatc tcaatattta ataatgaaat ttattttttt aattttaaaag caaataaaaag 1260  
cttaactttg aaccatggga aaaaaaaaaa aaaaaaaaaa aaaca 1305

<210> 71  
<211> 259  
<212> PRT  
<213> Homo sapiens

<400> 71

Met Asn Leu Val Asp Leu Trp Leu Thr Arg Ser Leu Ser Met Cys Leu  
 1 5 10 15  
 Leu Leu Gln Ser Phe Val Leu Met Ile Leu Cys Phe His Ser Ala Ser  
 20 25 30  
 Met Cys Pro Lys Gly Cys Leu Cys Ser Ser Ser Gly Gly Leu Asn Val  
 35 40 45  
 Thr Cys Ser Asn Ala Asn Leu Lys Glu Ile Pro Arg Asp Leu Pro Pro  
 50 55 60  
 Glu Thr Val Leu Leu Tyr Leu Asp Ser Asn Gln Ile Thr Ser Ile Pro  
 65 70 75 80  
 Asn Glu Ile Phe Lys Asp Leu His Gln Leu Arg Val Leu Asn Leu Ser  
 85 90 95  
 Lys Asn Gly Ile Glu Phe Ile Asp Glu His Ala Phe Lys Gly Val Ala  
 100 105 110  
 Glu Thr Leu Gln Thr Leu Asp Leu Ser Asp Asn Arg Ile Gln Ser Val  
 115 120 125  
 His Lys Asn Ala Phe Asn Asn Leu Lys Ala Arg Ala Arg Ile Ala Asn  
 130 135 140  
 Asn Pro Trp His Cys Asp Cys Thr Leu Gln Gln Val Leu Arg Ser Met  
 145 150 155 160  
 Ala Ser Asn His Glu Thr Ala His Asn Val Ile Cys Lys Thr Ser Val  
 165 170 175  
 Leu Asp Glu His Ala Gly Arg Pro Phe Leu Asn Ala Ala Asn Asp Ala  
 180 185 190  
 Asp Leu Cys Asn Leu Pro Lys Lys Thr Thr Asp Tyr Ala Met Leu Val  
 195 200 205  
 Thr Met Phe Gly Trp Phe Thr Met Val Ile Ser Tyr Val Val Tyr Tyr  
 210 215 220  
 Val Arg Gln Asn Gln Glu Asp Ala Arg Arg His Leu Glu Tyr Leu Lys  
 225 230 235 240  
 Ser Leu Pro Ser Arg Gln Lys Lys Ala Asp Glu Pro Asp Asp Ile Ser  
 245 250 255  
 Thr Val Val

&lt;210&gt; 72

&lt;211&gt; 2290



&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 72

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accgagccga ggcgaccgaa ggcgcgcgcg agatgcaggt gagcaagagg atgctggcgg 60
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tgctgggctc agtgctgtca ggctcggcca cgggctgccc gcccgcgtgc gactgctccg 180
cccaggaccg cgctgtgctg tgcacccgca agtgetttgt ggcagtcccc gagggcatcc 240
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agttcgccag cttcccgcac ctggaggagc tggagctcaa cgagaacatc gtgagcgccg 360
tggagccccg cgcttcaac aacctcttca acctccggac gctgggtctc cgcagcaacc 420
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&lt;210&gt; 73

&lt;211&gt; 620

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 73

Met Gln Val Ser Lys Arg Met Leu Ala Gly Gly Val Arg Ser Met Pro

1

5

10

15

Ser Pro Leu Leu Ala Cys Trp Gln Pro Ile Leu Leu Leu Val Leu Gly  
 20 25 30

Ser Val Leu Ser Gly Ser Ala Thr Gly Cys Pro Pro Arg Cys Glu Cys  
 35 40 45

Ser Ala Gln Asp Arg Ala Val Leu Cys His Arg Lys Cys Phe Val Ala  
 50 55 60

Val Pro Glu Gly Ile Pro Thr Glu Thr Arg Leu Leu Asp Leu Gly Lys  
 65 70 75 80

Asn Arg Ile Lys Thr Leu Asn Gln Asp Glu Phe Ala Ser Phe Pro His  
 85 90 95

Leu Glu Glu Leu Glu Leu Asn Glu Asn Ile Val Ser Ala Val Glu Pro  
 100 105 110

Gly Ala Phe Asn Asn Leu Phe Asn Leu Arg Thr Leu Gly Leu Arg Ser  
 115 120 125

Asn Arg Leu Lys Leu Ile Pro Leu Gly Val Phe Thr Gly Leu Ser Asn  
 130 135 140

Leu Thr Lys Gln Asp Ile Ser Glu Asn Lys Ile Val Ile Leu Leu Asp  
 145 150 155 160

Tyr Met Phe Gln Asp Leu Tyr Asn Leu Lys Ser Leu Glu Val Gly Asp  
 165 170 175

Asn Asp Leu Val Tyr Ile Ser His Arg Ala Phe Ser Gly Leu Asn Ser  
 180 185 190

Leu Glu Gln Leu Thr Leu Glu Lys Cys Asn Leu Thr Ser Ile Pro Thr  
 195 200 205

Glu Ala Leu Ser His Leu His Gly Leu Ile Val Leu Arg Leu Arg His  
 210 215 220

Leu Asn Ile Asn Ala Ile Arg Asp Tyr Ser Phe Lys Arg Leu Tyr Arg  
 225 230 235 240

Leu Lys Val Leu Glu Ile Ser His Trp Pro Tyr Leu Asp Thr Met Thr  
 245 250 255

Pro Asn Cys Leu Tyr Gly Leu Asn Leu Thr Ser Leu Ser Ile Thr His  
 260 265 270

Cys Asn Leu Thr Ala Val Pro Tyr Leu Ala Val Arg His Leu Val Tyr  
 275 280 285

Leu Arg Phe Leu Asn Leu Ser Tyr Asn Pro Ile Ser Thr Ile Glu Gly  
 290 295 300

Ser Met Leu His Glu Leu Leu Arg Leu Gln Glu Ile Gln Leu Val Gly  
 305 310 315 320  
 Gly Gln Leu Ala Val Val Glu Pro Tyr Ala Phe Arg Gly Leu Asn Tyr  
 325 330 335  
 Leu Arg Val Leu Asn Val Ser Gly Asn Gln Leu Thr Thr Leu Glu Glu  
 340 345 350  
 Ser Val Phe His Ser Val Gly Asn Leu Glu Thr Leu Ile Leu Asp Ser  
 355 360 365  
 Asn Pro Leu Ala Cys Asp Cys Arg Leu Leu Trp Val Phe Arg Arg Arg  
 370 375 380  
 Trp Arg Leu Asn Phe Asn Arg Gln Gln Pro Thr Cys Ala Thr Pro Glu  
 385 390 395 400  
 Phe Val Gln Gly Lys Glu Phe Lys Asp Phe Pro Asp Val Leu Leu Pro  
 405 410 415  
 Asn Tyr Phe Thr Cys Arg Arg Ala Arg Ile Arg Asp Arg Lys Ala Gln  
 420 425 430  
 Gln Val Phe Val Asp Glu Gly His Thr Val Gln Phe Val Cys Arg Ala  
 435 440 445  
 Asp Gly Asp Pro Pro Pro Ala Ile Leu Trp Leu Ser Pro Arg Lys His  
 450 455 460  
 Leu Val Ser Ala Lys Ser Asn Gly Arg Leu Thr Val Phe Pro Asp Gly  
 465 470 475 480  
 Thr Leu Glu Val Arg Tyr Ala Gln Val Gln Asp Asn Gly Thr Tyr Leu  
 485 490 495  
 Cys Ile Ala Ala Asn Ala Gly Gly Asn Asp Ser Met Pro Ala His Leu  
 500 505 510  
 His Val Arg Ser Tyr Ser Pro Asp Trp Pro His Gln Pro Asn Lys Thr  
 515 520 525  
 Phe Ala Phe Ile Ser Asn Gln Pro Gly Glu Gly Glu Ala Asn Ser Thr  
 530 535 540  
 Arg Ala Thr Val Pro Phe Pro Phe Asp Ile Lys Thr Leu Ile Ile Ala  
 545 550 555 560  
 Thr Thr Met Gly Phe Ile Ser Phe Leu Gly Val Val Leu Phe Cys Leu  
 565 570 575  
 Val Leu Leu Phe Leu Trp Ser Arg Gly Lys Gly Asn Thr Lys His Asn

580

585

590

Ile Glu Ile Glu Tyr Val Pro Arg Lys Ser Asp Ala Gly Ile Ser Ser  
           595                                600                                605

Ala Asp Ala Pro Arg Lys Phe Asn Met Lys Met Ile  
           610                                615                                620

&lt;210&gt; 74

&lt;211&gt; 22

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
           oligonucleotide probe

&lt;400&gt; 74

tcacctggag cctttattgg cc

22

&lt;210&gt; 75

&lt;211&gt; 23

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
           oligonucleotide probe

&lt;400&gt; 75

ataccagcta taaccaggct gcg

23

&lt;210&gt; 76

&lt;211&gt; 52

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
           oligonucleotide probe

&lt;400&gt; 76

caacagtaag tggtttgatg ctcttccaaa tctagagatt ctgatgattg  
           gg

50

52

&lt;210&gt; 77

&lt;211&gt; 22

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
           oligonucleotide probe

<400> 77  
 ccatgtgtct cctcctacaa ag 22  
  
 <210> 78  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe  
  
 <400> 78  
 gggaatagat gtgatctgat tgg 23  
  
 <210> 79  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe  
  
 <400> 79  
 cacctgtagc aatgcaaata tcaaggaaat acctagagat cttcctcctg 50  
  
 <210> 80  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe  
  
 <400> 80  
 agcaaccgcc tgaagctcat cc 22  
  
 <210> 81  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe  
  
 <400> 81  
 aaggcgcggt gaaagatgta gacg 24  
  
 <210> 82

<211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 82  
 gactacatgt ttcaggacct gtacaacctc aagtcactgg aggttggcga 50

<210> 83  
 <211> 1685  
 <212> DNA  
 <213> Homo sapiens

<400> 83  
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 agccaggag cggcgcgga agcgcgatgg gggccccagc cgctcctc ctgctcctgc 180  
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 agcccatcat cactgggtat aaatcttcat tacgggaaaa agacacagcc accctaaact 600  
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 aaaca 1685

<210> 84  
 <211> 398  
 <212> PRT  
 <213> Homo sapiens

<400> 84

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Cys	Cys	Trp	Ala 20	Pro	Gly	Gly	Ala	Asn 25	Leu	Ser	Gln	Asp	Asp 30	Ser	Gln
Pro	Trp	Thr 35	Ser	Asp	Glu	Thr	Val 40	Val	Ala	Gly	Gly	Thr 45	Val	Val	Leu
Lys 50	Cys	Gln	Val	Lys	Asp	His 55	Glu	Asp	Ser	Ser	Leu 60	Gln	Trp	Ser	Asn
Pro 65	Ala	Gln	Gln	Thr	Leu 70	Tyr	Phe	Gly	Glu	Lys 75	Arg	Ala	Leu	Arg	Asp 80
Asn	Arg	Ile	Gln 85	Leu	Val	Thr	Ser	Thr	Pro 90	His	Glu	Leu	Ser	Ile 95	Ser
Ile	Ser	Asn 100	Val	Ala	Leu	Ala	Asp	Glu 105	Gly	Glu	Tyr	Thr 110	Cys	Ser	Ile
Phe	Thr	Met 115	Pro	Val	Arg	Thr	Ala 120	Lys	Ser	Leu	Val 125	Thr	Val	Leu	Gly
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Lys 145	Asp	Thr	Ala	Thr 150	Leu	Asn	Cys	Gln	Ser	Ser 155	Gly	Ser	Lys	Pro	Ala 160
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Ser	Val 195	Thr	Phe	Gln	Val	Thr 200	Arg	Glu	Asp	Asp	Gly 205	Ala	Ser	Ile	Val
Cys 210	Ser	Val	Asn	His 215	Glu	Ser	Leu	Lys	Gly	Ala 220	Asp	Arg	Ser	Thr	Ser
Gln 225	Arg	Ile	Glu	Val 230	Leu	Tyr	Thr	Pro	Thr	Ala 235	Met	Ile	Arg	Pro	Asp 240
Pro	Pro	His	Pro 245	Arg	Glu	Gly	Gln	Lys	Leu 250	Leu	Leu	His	Cys	Glu 255	Gly
Arg	Gly	Asn 260	Pro	Val	Pro	Gln	Gln	Tyr 265	Leu	Trp	Glu	Lys 270	Glu	Gly	Ser
Val	Pro 275	Pro	Leu	Lys	Met	Thr 280	Gln	Glu	Ser	Ala	Leu 285	Ile	Phe	Pro	Phe

Leu Asn Lys Ser Asp Ser Gly Thr Tyr Gly Cys Thr Ala Thr Ser Asn  
 290 295 300

Met Gly Ser Tyr Lys Ala Tyr Tyr Thr Leu Asn Val Asn Asp Pro Ser  
 305 310 315 320

Pro Val Pro Ser Ser Ser Ser Thr Tyr His Ala Ile Ile Gly Gly Ile  
 325 330 335

Val Ala Phe Ile Val Phe Leu Leu Leu Ile Met Leu Ile Phe Leu Gly  
 340 345 350

His Tyr Leu Ile Arg His Lys Gly Thr Tyr Leu Thr His Glu Ala Lys  
 355 360 365

Gly Ser Asp Asp Ala Pro Asp Ala Asp Thr Ala Ile Ile Asn Ala Glu  
 370 375 380

Gly Gly Gln Ser Gly Gly Asp Asp Lys Lys Glu Tyr Phe Ile  
 385 390 395

<210> 85

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 85

gctaggaatt ccacagaagc cc

22

<210> 86

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 86

aacctggaat gtcaccgagc tg

22

<210> 87

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic



## oligonucleotide probe

&lt;400&gt; 87

cctagcacag tgacgaggga cttggc

26

&lt;210&gt; 88

&lt;211&gt; 50

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 88

aagacacagc caccctaaac tgtcagtctt ctgggagcaa gcctgcagcc

50

&lt;210&gt; 89

&lt;211&gt; 50

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 89

gccttggcag acgagggcga gtacacctgc tcaatcttca ctatgcctgt

50

&lt;210&gt; 90

&lt;211&gt; 2755

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 90

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&lt;210&gt; 91

&lt;211&gt; 696

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 91

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Met Leu Leu Trp Ile Leu Leu Leu Glu Thr Ser Leu Cys Phe Ala Ala
  1                      5                      10                      15

```

```

Gly Asn Val Thr Gly Asp Val Cys Lys Glu Lys Ile Cys Ser Cys Asn
          20                      25                      30

```

```

Glu Ile Glu Gly Asp Leu His Val Asp Cys Glu Lys Lys Gly Phe Thr
          35                      40                      45

```

```

Ser Leu Gln Arg Phe Thr Ala Pro Thr Ser Gln Phe Tyr His Leu Phe
          50                      55                      60

```

```

Leu His Gly Asn Ser Leu Thr Arg Leu Phe Pro Asn Glu Phe Ala Asn
          65                      70                      75                      80

```

```

Phe Tyr Asn Ala Val Ser Leu His Met Glu Asn Asn Gly Leu His Glu
          85                      90                      95

```

Ile Val Pro Gly Ala Phe Leu Gly Leu Gln Leu Val Lys Arg Leu His  
 100 105 110  
 Ile Asn Asn Asn Lys Ile Lys Ser Phe Arg Lys Gln Thr Phe Leu Gly  
 115 120 125  
 Leu Asp Asp Leu Glu Tyr Leu Gln Ala Asp Phe Asn Leu Leu Arg Asp  
 130 135 140  
 Ile Asp Pro Gly Ala Phe Gln Asp Leu Asn Lys Leu Glu Val Leu Ile  
 145 150 155 160  
 Leu Asn Asp Asn Leu Ile Ser Thr Leu Pro Ala Asn Val Phe Gln Tyr  
 165 170 175  
 Val Pro Ile Thr His Leu Asp Leu Arg Gly Asn Arg Leu Lys Thr Leu  
 180 185 190  
 Pro Tyr Glu Glu Val Leu Glu Gln Ile Pro Gly Ile Ala Glu Ile Leu  
 195 200 205  
 Leu Glu Asp Asn Pro Trp Asp Cys Thr Cys Asp Leu Leu Ser Leu Lys  
 210 215 220  
 Glu Trp Leu Glu Asn Ile Pro Lys Asn Ala Leu Ile Gly Arg Val Val  
 225 230 235 240  
 Cys Glu Ala Pro Thr Arg Leu Gln Gly Lys Asp Leu Asn Glu Thr Thr  
 245 250 255  
 Glu Gln Asp Leu Cys Pro Leu Lys Asn Arg Val Asp Ser Ser Leu Pro  
 260 265 270  
 Ala Pro Pro Ala Gln Glu Glu Thr Phe Ala Pro Gly Pro Leu Pro Thr  
 275 280 285  
 Pro Phe Lys Thr Asn Gly Gln Glu Asp His Ala Thr Pro Gly Ser Ala  
 290 295 300  
 Pro Asn Gly Gly Thr Lys Ile Pro Gly Asn Trp Gln Ile Lys Ile Arg  
 305 310 315 320  
 Pro Thr Ala Ala Ile Ala Thr Gly Ser Ser Arg Asn Lys Pro Leu Ala  
 325 330 335  
 Asn Ser Leu Pro Cys Pro Gly Gly Cys Ser Cys Asp His Ile Pro Gly  
 340 345 350  
 Ser Gly Leu Lys Met Asn Cys Asn Asn Arg Asn Val Ser Ser Leu Ala  
 355 360 365  
 Asp Leu Lys Pro Lys Leu Ser Asn Val Gln Glu Leu Phe Leu Arg Asp  
 370 375 380

Asn Lys Ile His Ser Ile Arg Lys Ser His Phe Val Asp Tyr Lys Asn  
 385 390 395 400  
 Leu Ile Leu Leu Asp Leu Gly Asn Asn Asn Ile Ala Thr Val Glu Asn  
 405 410 415  
 Asn Thr Phe Lys Asn Leu Leu Asp Leu Arg Trp Leu Tyr Met Asp Ser  
 420 425 430  
 Asn Tyr Leu Asp Thr Leu Ser Arg Glu Lys Phe Ala Gly Leu Gln Asn  
 435 440 445  
 Leu Glu Tyr Leu Asn Val Glu Tyr Asn Ala Ile Gln Leu Ile Leu Pro  
 450 455 460  
 Gly Thr Phe Asn Ala Met Pro Lys Leu Arg Ile Leu Ile Leu Asn Asn  
 465 470 475 480  
 Asn Leu Leu Arg Ser Leu Pro Val Asp Val Phe Ala Gly Val Ser Leu  
 485 490 495  
 Ser Lys Leu Ser Leu His Asn Asn Tyr Phe Met Tyr Leu Pro Val Ala  
 500 505 510  
 Gly Val Leu Asp Gln Leu Thr Ser Ile Ile Gln Ile Asp Leu His Gly  
 515 520 525  
 Asn Pro Trp Glu Cys Ser Cys Thr Ile Val Pro Phe Lys Gln Trp Ala  
 530 535 540  
 Glu Arg Leu Gly Ser Glu Val Leu Met Ser Asp Leu Lys Cys Glu Thr  
 545 550 555 560  
 Pro Val Asn Phe Phe Arg Lys Asp Phe Met Leu Leu Ser Asn Asp Glu  
 565 570 575  
 Ile Cys Pro Gln Leu Tyr Ala Arg Ile Ser Pro Thr Leu Thr Ser His  
 580 585 590  
 Ser Lys Asn Ser Thr Gly Leu Ala Glu Thr Gly Thr His Ser Asn Ser  
 595 600 605  
 Tyr Leu Asp Thr Ser Arg Val Ser Ile Ser Val Leu Val Pro Gly Leu  
 610 615 620  
 Leu Leu Val Phe Val Thr Ser Ala Phe Thr Val Val Gly Met Leu Val  
 625 630 635 640  
 Phe Ile Leu Arg Asn Arg Lys Arg Ser Lys Arg Arg Asp Ala Asn Ser  
 645 650 655  
 Ser Ala Ser Glu Ile Asn Ser Leu Gln Thr Val Cys Asp Ser Ser Tyr

660

665

670

Trp His Asn Gly Pro Tyr Asn Ala Asp Gly Ala His Arg Val Tyr Asp  
           675                                680                                685

Cys Gly Ser His Ser Leu Ser Asp  
       690                                695

&lt;210&gt; 92

&lt;211&gt; 22

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
           oligonucleotide probe

&lt;400&gt; 92

gttggatctg ggcaacaata ac

22

&lt;210&gt; 93

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
           oligonucleotide probe

&lt;400&gt; 93

attggttgtagc aggctgagtt taag

24

&lt;210&gt; 94

&lt;211&gt; 45

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
           oligonucleotide probe

&lt;400&gt; 94

ggtggctata catgtagc aattacctgg acacgctgtc ccggg

45

&lt;210&gt; 95

&lt;211&gt; 2226

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 95

agtcgactgc gtccctgta cccggcgcca gctgtgttc tgaccccaga ataactcagg 60  
 gctgcaccgg gctggcagc gctccgcaca catttctgt cgcggcctaa gggaaactgt 120  
 tggcgcgtgg gcccgcgggg ggattcttgg cagttggggg gtccgtcggg agcgagggcg 180

```

gaggggaagg gaggggaac cgggttgggg aagccagctg tagagggcgg tgaccgcgct 240
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gttgat 2226

```

&lt;210&gt; 96

&lt;211&gt; 490

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 96

```

Met Arg Pro Ala Phe Ala Leu Cys Leu Leu Trp Gln Ala Leu Trp Pro
  1              5              10              15

```

```

Gly Pro Gly Gly Gly Glu His Pro Thr Ala Asp Arg Ala Gly Cys Ser
          20              25              30

```

```

Ala Ser Gly Ala Cys Tyr Ser Leu His His Ala Thr Met Lys Arg Gln
    35              40              45

```

```

Ala Ala Glu Glu Ala Cys Ile Leu Arg Gly Gly Ala Leu Ser Thr Val
    50              55              60

```

Arg	Ala	Gly	Ala	Glu	Leu	Arg	Ala	Val	Leu	Ala	Leu	Leu	Arg	Ala	Gly	65	70	75	80
Pro	Gly	Pro	Gly	Gly	Gly	Ser	Lys	Asp	Leu	Leu	Phe	Trp	Val	Ala	Leu	85	90	95	
Glu	Arg	Arg	Arg	Ser	His	Cys	Thr	Leu	Glu	Asn	Glu	Pro	Leu	Arg	Gly	100	105	110	
Phe	Ser	Trp	Leu	Ser	Ser	Asp	Pro	Gly	Gly	Leu	Glu	Ser	Asp	Thr	Leu	115	120	125	
Gln	Trp	Val	Glu	Glu	Pro	Gln	Arg	Ser	Cys	Thr	Ala	Arg	Arg	Cys	Ala	130	135	140	
Val	Leu	Gln	Ala	Thr	Gly	Gly	Val	Glu	Pro	Ala	Gly	Trp	Lys	Glu	Met	145	150	155	160
Arg	Cys	His	Leu	Arg	Ala	Asn	Gly	Tyr	Leu	Cys	Lys	Tyr	Gln	Phe	Glu	165	170	175	
Val	Leu	Cys	Pro	Ala	Pro	Arg	Pro	Gly	Ala	Ala	Ser	Asn	Leu	Ser	Tyr	180	185	190	
Arg	Ala	Pro	Phe	Gln	Leu	His	Ser	Ala	Ala	Leu	Asp	Phe	Ser	Pro	Pro	195	200	205	
Gly	Thr	Glu	Val	Ser	Ala	Leu	Cys	Arg	Gly	Gln	Leu	Pro	Ile	Ser	Val	210	215	220	
Thr	Cys	Ile	Ala	Asp	Glu	Ile	Gly	Ala	Arg	Trp	Asp	Lys	Leu	Ser	Gly	225	230	235	240
Asp	Val	Leu	Cys	Pro	Cys	Pro	Gly	Arg	Tyr	Leu	Arg	Ala	Gly	Lys	Cys	245	250	255	
Ala	Glu	Leu	Pro	Asn	Cys	Leu	Asp	Asp	Leu	Gly	Gly	Phe	Ala	Cys	Glu	260	265	270	
Cys	Ala	Thr	Gly	Phe	Glu	Leu	Gly	Lys	Asp	Gly	Arg	Ser	Cys	Val	Thr	275	280	285	
Ser	Gly	Glu	Gly	Gln	Pro	Thr	Leu	Gly	Gly	Thr	Gly	Val	Pro	Thr	Arg	290	295	300	
Arg	Pro	Pro	Ala	Thr	Ala	Thr	Ser	Pro	Val	Pro	Gln	Arg	Thr	Trp	Pro	305	310	315	320
Ile	Arg	Val	Asp	Glu	Lys	Leu	Gly	Glu	Thr	Pro	Leu	Val	Pro	Glu	Gln	325	330	335	
Asp	Asn	Ser	Val	Thr	Ser	Ile	Pro	Glu	Ile	Pro	Arg	Trp	Gly	Ser	Gln				

340	345	350
Ser Thr Met Ser Thr Leu Gln Met Ser Leu Gln Ala Glu Ser Lys Ala		
355	360	365
Thr Ile Thr Pro Ser Gly Ser Val Ile Ser Lys Phe Asn Ser Thr Thr		
370	375	380
Ser Ser Ala Thr Pro Gln Ala Phe Asp Ser Ser Ser Ala Val Val Phe		
385	390	395
Ile Phe Val Ser Thr Ala Val Val Val Leu Val Ile Leu Thr Met Thr		
405	410	415
Val Leu Gly Leu Val Lys Leu Cys Phe His Glu Ser Pro Ser Ser Gln		
420	425	430
Pro Arg Lys Glu Ser Met Gly Pro Pro Gly Leu Glu Ser Asp Pro Glu		
435	440	445
Pro Ala Ala Leu Gly Ser Ser Ser Ala His Cys Thr Asn Asn Gly Val		
450	455	460
Lys Val Gly Asp Cys Asp Leu Arg Asp Arg Ala Glu Gly Ala Leu Leu		
465	470	475
Ala Glu Ser Pro Leu Gly Ser Ser Asp Ala		
485	490	

&lt;210&gt; 97

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 97

tggaaggaga tgcgatgcca cctg

24

&lt;210&gt; 98

&lt;211&gt; 20

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 98

tgaccagtgg ggaaggacag

20



<210> 99  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 99  
 acagagcaga gggcgcttg 20

<210> 100  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 100  
 tcagggacaa gtggtgtctc tccc 24

<210> 101  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 101  
 tcaggggaagg agtgtgcagt tctg 24

<210> 102  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 102  
 acagctcccg atctcagtta cttgcatcgc ggacgaaatc ggcgctcgct 50

<210> 103  
 <211> 2026  
 <212> DNA  
 <213> Homo sapiens

&lt;400&gt; 103

```

cggaacgggtg ggattcagca gtggcctgtg gctgccagag cagctcctca ggggaaacta 60
agcgtcgagt cagacggcac cataatcgcc tttaaaagtg cctccgcect gccggccgcg 120
tatccccggg ctacctgggc cgccccggcg cgggtgcgcgc gtgagagggg gcgcgcgggc 180
agcggagcgc cgggtgtgagc cagcgtgtgt gccagtgtga gcggcggtgt gagcgcggtg 240
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gctgccatga ggggcgcgaa cgccgtgggc ccactctgcc tgctgctggc tgccgccacc 360
cagctctcgc ggcagcagtc ccagagaga cctgttttca catgtggtgg cattcttact 420
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gtgttatttg tttcaccttc aagcctttgc cctgaggtgt tacaatcttg tcttgcgttt 1980
tctaaatcaa tgcttaataa aatattttta aaggaaaaaa aaaaaa 2026

```

&lt;210&gt; 104

&lt;211&gt; 415

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 104

```

Met Arg Gly Ala Asn Ala Trp Ala Pro Leu Cys Leu Leu Leu Ala Ala
  1             5             10             15

```

```

Ala Thr Gln Leu Ser Arg Gln Gln Ser Pro Glu Arg Pro Val Phe Thr
      20             25             30

```

```

Cys Gly Gly Ile Leu Thr Gly Glu Ser Gly Phe Ile Gly Ser Glu Gly
      35             40             45

```

```

Phe Pro Gly Val Tyr Pro Pro Asn Ser Lys Cys Thr Trp Lys Ile Thr
      50             55             60

```

Val Pro Glu Gly Lys Val Val Val Leu Asn Phe Arg Phe Ile Asp Leu  
 65 70 75 80  
 Glu Ser Asp Asn Leu Cys Arg Tyr Asp Phe Val Asp Val Tyr Asn Gly  
 85 90 95  
 His Ala Asn Gly Gln Arg Ile Gly Arg Phe Cys Gly Thr Phe Arg Pro  
 100 105 110  
 Gly Ala Leu Val Ser Ser Gly Asn Lys Met Met Val Gln Met Ile Ser  
 115 120 125  
 Asp Ala Asn Thr Ala Gly Asn Gly Phe Met Ala Met Phe Ser Ala Ala  
 130 135 140  
 Glu Pro Asn Glu Arg Gly Asp Gln Tyr Cys Gly Gly Leu Leu Asp Arg  
 145 150 155 160  
 Pro Ser Gly Ser Phe Lys Thr Pro Asn Trp Pro Asp Arg Asp Tyr Pro  
 165 170 175  
 Ala Gly Val Thr Cys Val Trp His Ile Val Ala Pro Lys Asn Gln Leu  
 180 185 190  
 Ile Glu Leu Lys Phe Glu Lys Phe Asp Val Glu Arg Asp Asn Tyr Cys  
 195 200 205  
 Arg Tyr Asp Tyr Val Ala Val Phe Asn Gly Gly Glu Val Asn Asp Ala  
 210 215 220  
 Arg Arg Ile Gly Lys Tyr Cys Gly Asp Ser Pro Pro Ala Pro Ile Val  
 225 230 235 240  
 Ser Glu Arg Asn Glu Leu Leu Ile Gln Phe Leu Ser Asp Leu Ser Leu  
 245 250 255  
 Thr Ala Asp Gly Phe Ile Gly His Tyr Ile Phe Arg Pro Lys Lys Leu  
 260 265 270  
 Pro Thr Thr Thr Glu Gln Pro Val Thr Thr Thr Phe Pro Val Thr Thr  
 275 280 285  
 Gly Leu Lys Pro Thr Val Ala Leu Cys Gln Gln Lys Cys Arg Arg Thr  
 290 295 300  
 Gly Thr Leu Glu Gly Asn Tyr Cys Ser Ser Asp Phe Val Leu Ala Gly  
 305 310 315 320  
 Thr Val Ile Thr Thr Ile Thr Arg Asp Gly Ser Leu His Ala Thr Val  
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 Ser Ile Ile Asn Ile Tyr Lys Glu Gly Asn Leu Ala Ile Gln Gln Ala

340	345	350
Gly Lys Asn Met Ser Ala Arg Leu Thr Val Val Cys Lys Gln Cys Pro		
355	360	365
Leu Leu Arg Arg Gly Leu Asn Tyr Ile Ile Met Gly Gln Val Gly Glu		
370	375	380
Asp Gly Arg Gly Lys Ile Met Pro Asn Ser Phe Ile Met Met Phe Lys		
385	390	395 400
Thr Lys Asn Gln Lys Leu Leu Asp Ala Leu Lys Asn Lys Gln Cys		
405	410	415

&lt;210&gt; 105

&lt;211&gt; 22

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 105

ccgattcata gacctcgaga gt

22

&lt;210&gt; 106

&lt;211&gt; 22

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 106

gtcaaggagt cctccacaat ac

22

&lt;210&gt; 107

&lt;211&gt; 45

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 107

gtgtacaatg gccatgccaa tggccagcgc attggccgct tctgt

45

&lt;210&gt; 108

&lt;211&gt; 1838

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 108

```

cggacgcgtg ggcggacgcg tgggcggccc acggcgcgcc cgggctgggg cggtcgcttc 60
ttccttctcc gtggcctaag aggggtcccca gectgggtaa agatggcccc atggcccccg 120
aagggcctag tcccagctgt gctctggggc ctcagcctct tcctcaacct cccaggacct 180
atctggctcc agccctctcc acctccccag tcttctcccc cgctcagcc ccatccgtgt 240
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aactttggag gtggaaacac tgctggggag gaagagaatt tgtccaaata caaagacagt 360
gagaccgcgc ttgtagaggt gctggagggg gtgtgcagca agtcagactt cgagtgccac 420
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gataccatga gctcttcacc tggcggggac tggcaggctt cacaatgtgt gaatttcaaa 1620
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acaggggtgg ggccatcaca gctccctcct gccagctgca tgctgccagt tctgttctg 1740
tgttaccac atccccacac ccattgccca cttatttatt catctcagga aataaagaaa 1800
ggtcttgga agttaaaaaa aaaaaaaaaa aaaaaaaa 1838

```

&lt;210&gt; 109

&lt;211&gt; 420

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 109

```

Met Ala Pro Trp Pro Pro Lys Gly Leu Val Pro Ala Val Leu Trp Gly
  1              5              10              15

Leu Ser Leu Phe Leu Asn Leu Pro Gly Pro Ile Trp Leu Gln Pro Ser
      20              25              30

Pro Pro Pro Gln Ser Ser Pro Pro Pro Gln Pro His Pro Cys His Thr
      35              40              45

Cys Arg Gly Leu Val Asp Ser Phe Asn Lys Gly Leu Glu Arg Thr Ile
      50              55              60

```

Arg Asp Asn Phe Gly Gly Gly Asn Thr Ala Trp Glu Glu Glu Asn Leu  
 65 70 75 80  
 Ser Lys Tyr Lys Asp Ser Glu Thr Arg Leu Val Glu Val Leu Glu Gly  
 85 90 95  
 Val Cys Ser Lys Ser Asp Phe Glu Cys His Arg Leu Leu Glu Leu Ser  
 100 105 110  
 Glu Glu Leu Val Glu Ser Trp Trp Phe His Lys Gln Gln Glu Ala Pro  
 115 120 125  
 Asp Leu Phe Gln Trp Leu Cys Ser Asp Ser Leu Lys Leu Cys Cys Pro  
 130 135 140  
 Ala Gly Thr Phe Gly Pro Ser Cys Leu Pro Cys Pro Gly Gly Thr Glu  
 145 150 155 160  
 Arg Pro Cys Gly Gly Tyr Gly Gln Cys Glu Gly Glu Gly Thr Arg Gly  
 165 170 175  
 Gly Ser Gly His Cys Asp Cys Gln Ala Gly Tyr Gly Gly Glu Ala Cys  
 180 185 190  
 Gly Gln Cys Gly Leu Gly Tyr Phe Glu Ala Glu Arg Asn Ala Ser His  
 195 200 205  
 Leu Val Cys Ser Ala Cys Phe Gly Pro Cys Ala Arg Cys Ser Gly Pro  
 210 215 220  
 Glu Glu Ser Asn Cys Leu Gln Cys Lys Lys Gly Trp Ala Leu His His  
 225 230 235 240  
 Leu Lys Cys Val Asp Ile Asp Glu Cys Gly Thr Glu Gly Ala Asn Cys  
 245 250 255  
 Gly Ala Asp Gln Phe Cys Val Asn Thr Glu Gly Ser Tyr Glu Cys Arg  
 260 265 270  
 Asp Cys Ala Lys Ala Cys Leu Gly Cys Met Gly Ala Gly Pro Gly Arg  
 275 280 285  
 Cys Lys Lys Cys Ser Pro Gly Tyr Gln Gln Val Gly Ser Lys Cys Leu  
 290 295 300  
 Asp Val Asp Glu Cys Glu Thr Glu Val Cys Pro Gly Glu Asn Lys Gln  
 305 310 315 320  
 Cys Glu Asn Thr Glu Gly Gly Tyr Arg Cys Ile Cys Ala Glu Gly Tyr  
 325 330 335  
 Lys Gln Met Glu Gly Ile Cys Val Lys Glu Gln Ile Pro Glu Ser Ala  
 340 345 350

Gly Phe Phe Ser Glu Met Thr Glu Asp Glu Leu Val Val Leu Gln Gln  
           355                                  360                                  365

Met Phe Phe Gly Ile Ile Ile Cys Ala Leu Ala Thr Leu Ala Ala Lys  
      370                                  375                                  380

Gly Asp Leu Val Phe Thr Ala Ile Phe Ile Gly Ala Val Ala Ala Met  
 385                                  390                                  395                                  400

Thr Gly Tyr Trp Leu Ser Glu Arg Ser Asp Arg Val Leu Glu Gly Phe  
                                   405                                  410                                  415

Ile Lys Gly Arg  
                   420

<210> 110

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
           oligonucleotide probe

<400> 110

cctggctatc agcaggtggg ctccaagtgt ctcgatgtgg atgagtgtga

50

<210> 111

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
           oligonucleotide probe

<400> 111

attctgcgtg aacactgagg gc

22

<210> 112

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
           oligonucleotide probe

<400> 112

atctgcttgt agccctcggc ac

22

<210> 113

<211> 1616  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> modified\_base  
 <222> (1461)  
 <223> a, t, c or g

```

<400> 113
tgagaccctc ctgcagcctt ctcaagggac agcccccactc tgccctcttgc tctccaggg 60
cagcaccatg cagccccctgt ggctctgctg ggcactcttg gtgttgcccc tggccagccc 120
cggggccgcc ctgaccgggg agcagctcct gggcagcctg ctgcggcagc tgcagctcaa 180
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cagccagagc ttccgagagg tggccggcag gttcctggcg ttggaggcca gcacacacct 360
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gcggtctctt caggagccgg tccccaggc cgcgtctgcac aggcacgggc ggctgtcccc 480
gcgcagcgcc cgggccgggg tgaccgtcga gtggtctgcg gtccgcgacg acgggtccaa 540
ccgcacctcc ctcatcgact ccaggctggt gtccgtccac gagagcggct ggaaggcctt 600
cgacgtgacc gaggccgtga acttctggca gcagctgagc cggccccggc agcgcgtgct 660
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gtgtgtgttt ctgaagtgtt cgagggtacc aggagagctg gcgatgactg aactgctgat 1260
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aaagtccctc accaccactc tggacctaa acctgggggt aagtgtgggt tgtgcatccc 1560
caatccagat aataaagact ttgtaaaaca tgaataaaac acattttatt ctaaaa 1616

```

<210> 114  
 <211> 366  
 <212> PRT  
 <213> Homo sapiens

```

<400> 114
Met Gln Pro Leu Trp Leu Cys Trp Ala Leu Trp Val Leu Pro Leu Ala
  1                      5                      10                      15

Ser Pro Gly Ala Ala Leu Thr Gly Glu Gln Leu Leu Gly Ser Leu Leu
          20                      25                      30

Arg Gln Leu Gln Leu Lys Glu Val Pro Thr Leu Asp Arg Ala Asp Met
          35                      40                      45

```



Glu Glu Leu Val Ile Pro Thr His Val Arg Ala Gln Tyr Val Ala Leu  
 50 55 60  
 Leu Gln Arg Ser His Gly Asp Arg Ser Arg Gly Lys Arg Phe Ser Gln  
 65 70 75 80  
 Ser Phe Arg Glu Val Ala Gly Arg Phe Leu Ala Leu Glu Ala Ser Thr  
 85 90 95  
 His Leu Leu Val Phe Gly Met Glu Gln Arg Leu Pro Pro Asn Ser Glu  
 100 105 110  
 Leu Val Gln Ala Val Leu Arg Leu Phe Gln Glu Pro Val Pro Lys Ala  
 115 120 125  
 Ala Leu His Arg His Gly Arg Leu Ser Pro Arg Ser Ala Arg Ala Arg  
 130 135 140  
 Val Thr Val Glu Trp Leu Arg Val Arg Asp Asp Gly Ser Asn Arg Thr  
 145 150 155 160  
 Ser Leu Ile Asp Ser Arg Leu Val Ser Val His Glu Ser Gly Trp Lys  
 165 170 175  
 Ala Phe Asp Val Thr Glu Ala Val Asn Phe Trp Gln Gln Leu Ser Arg  
 180 185 190  
 Pro Arg Gln Pro Leu Leu Leu Gln Val Ser Val Gln Arg Glu His Leu  
 195 200 205  
 Gly Pro Leu Ala Ser Gly Ala His Lys Leu Val Arg Phe Ala Ser Gln  
 210 215 220  
 Gly Ala Pro Ala Gly Leu Gly Glu Pro Gln Leu Glu Leu His Thr Leu  
 225 230 235 240  
 Asp Leu Gly Asp Tyr Gly Ala Gln Gly Asp Cys Asp Pro Glu Ala Pro  
 245 250 255  
 Met Thr Glu Gly Thr Arg Cys Cys Arg Gln Glu Met Tyr Ile Asp Leu  
 260 265 270  
 Gln Gly Met Lys Trp Ala Glu Asn Trp Val Leu Glu Pro Pro Gly Phe  
 275 280 285  
 Leu Ala Tyr Glu Cys Val Gly Thr Cys Arg Gln Pro Pro Glu Ala Leu  
 290 295 300  
 Ala Phe Lys Trp Pro Phe Leu Gly Pro Arg Gln Cys Ile Ala Ser Glu  
 305 310 315 320  
 Thr Asp Ser Leu Pro Met Ile Val Ser Ile Lys Glu Gly Gly Arg Thr  
 325 330 335

Arg Pro Gln Val Val Ser Leu Pro Asn Met Arg Val Gln Lys Cys Ser  
                   340                  345                  350

Cys Ala Ser Asp Gly Ala Leu Val Pro Arg Arg Leu Gln Pro  
           355                  360                  365

<210> 115  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
           oligonucleotide probe

<400> 115  
 aggactgccca taacttgcct g 21

<210> 116  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
           oligonucleotide probe

<400> 116  
 ataggagttg aagcagcgct gc 22

<210> 117  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
           oligonucleotide probe

<400> 117  
 tgtgtggaca tagacgagtg ccgctaccgc tactgccagc accgc 45

<210> 118  
 <211> 1857  
 <212> DNA  
 <213> Homo sapiens

<400> 118  
 gtctgttccc aggagtcctt cggcggtgtgt tgtgtcagtg gcctgatcgc gatgggggaca 60  
 aaggcgcaag tcgagaggaa actgttgtgc ctcttcatat tggcgatcct gttgtgctcc 120  
 ctggcattgg gcagtgttac agtgactct tctgaacctg aagtcagaat tcttgagaat 180

```

aatcctgtga agttgtcctg tgcctactcg ggcttttctt ctccccgtgt ggagtgggaag 240
tttgaccaag gagacaccac cagactcggt tgctataata acaagatcac agcttccat 300
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accgctgctc taaagaaaag aaaactggag gctgggcgca gtggctcacg cctgtaatcc 1680
cagaggctga ggcaggcgga tcacctgagg tggggagtgc gggatcagcc tgaccaacat 1740
ggagaaaccc tactggaaat acaaagttag ccaggcatgg tgggtgcatgc ctgtagtccc 1800
agctgctcag gagcctggca acaagagcaa aactccagct caaaaaaaaa aaaaaaa 1857

```

&lt;210&gt; 119

&lt;211&gt; 299

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 119

```

Met Gly Thr Lys Ala Gln Val Glu Arg Lys Leu Leu Cys Leu Phe Ile
  1                      5                      10                      15

```

```

Leu Ala Ile Leu Leu Cys Ser Leu Ala Leu Gly Ser Val Thr Val His
          20                      25                      30

```

```

Ser Ser Glu Pro Glu Val Arg Ile Pro Glu Asn Asn Pro Val Lys Leu
          35                      40                      45

```

```

Ser Cys Ala Tyr Ser Gly Phe Ser Ser Pro Arg Val Glu Trp Lys Phe
          50                      55                      60

```

```

Asp Gln Gly Asp Thr Thr Arg Leu Val Cys Tyr Asn Asn Lys Ile Thr
          65                      70                      75                      80

```

```

Ala Ser Tyr Glu Asp Arg Val Thr Phe Leu Pro Thr Gly Ile Thr Phe
          85                      90                      95

```

Lys Ser Val Thr Arg Glu Asp Thr Gly Thr Tyr Thr Cys Met Val Ser  
 100 105 110  
 Glu Glu Gly Gly Asn Ser Tyr Gly Glu Val Lys Val Lys Leu Ile Val  
 115 120 125  
 Leu Val Pro Pro Ser Lys Pro Thr Val Asn Ile Pro Ser Ser Ala Thr  
 130 135 140  
 Ile Gly Asn Arg Ala Val Leu Thr Cys Ser Glu Gln Asp Gly Ser Pro  
 145 150 155 160  
 Pro Ser Glu Tyr Thr Trp Phe Lys Asp Gly Ile Val Met Pro Thr Asn  
 165 170 175  
 Pro Lys Ser Thr Arg Ala Phe Ser Asn Ser Ser Tyr Val Leu Asn Pro  
 180 185 190  
 Thr Thr Gly Glu Leu Val Phe Asp Pro Leu Ser Ala Ser Asp Thr Gly  
 195 200 205  
 Glu Tyr Ser Cys Glu Ala Arg Asn Gly Tyr Gly Thr Pro Met Thr Ser  
 210 215 220  
 Asn Ala Val Arg Met Glu Ala Val Glu Arg Asn Val Gly Val Ile Val  
 225 230 235 240  
 Ala Ala Val Leu Val Thr Leu Ile Leu Leu Gly Ile Leu Val Phe Gly  
 245 250 255  
 Ile Trp Phe Ala Tyr Ser Arg Gly His Phe Asp Arg Thr Lys Lys Gly  
 260 265 270  
 Thr Ser Ser Lys Lys Val Ile Tyr Ser Gln Pro Ser Ala Arg Ser Glu  
 275 280 285  
 Gly Glu Phe Lys Gln Thr Ser Ser Phe Leu Val  
 290 295

&lt;210&gt; 120

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

&lt;400&gt; 120

tcgcggagct gtgttctgtt tccc

24

&lt;210&gt; 121

&lt;211&gt; 50

<212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 121  
 tgatcgcat ggggacaaag gcgcaagctc gagaggaaac tgttgtgcct 50

<210> 122  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 122  
 acacctgggtt caaagatggg 20

<210> 123  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 123  
 taggaagagt tgctgaaggc acgg 24

<210> 124  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 124  
 ttgccttact caggtgctac 20

<210> 125  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic

## oligonucleotide probe

<400> 125  
actcagcagt ggtaggaaag

20

<210> 126  
<211> 1210  
<212> DNA  
<213> Homo sapiens

<400> 126  
cagcgcgtgg cgggcgcgcg tgtggggaca gcatgagcgg cgggttggatg gcgcagggttg 60  
gagcgtggcg aacagggggt ctgggcctgg cgctgctgct gctgctcggc ctcggaactag 120  
gcctggaggc cgcgcgcgag ccgctttcca ccccgacctc tgcccaggcc gcaggcccca 180  
gctcaggctc gtgcccaccc accaagttcc agtgccgcac cagtggetta tgcgtgcccc 240  
tcacctggcg ctgcgacagg gacttggact gcagcgatgg cagcgatgag gaggagtga 300  
ggattgagcc atgtaccag aaagggaat gccaccgcc cctggcctc cctgcccct 360  
gcaccggcgt cagtactgc tctgggggaa ctgacaagaa actgcgcaac tgcagccgcc 420  
tgccctgcct agcaggcgag ctccgttgca cgctgagcga tgactgcatt ccactcacgt 480  
ggcctgcga cggccacca gactgtcccg actccagcga cgagctcggc tgtggaacca 540  
atgagatcct cccggaagg gatgccaca ccatggggcc cctgtgacc ctggagagt 600  
tcacctctct caggaatgcc acaaccatgg ggcacctgt gacctggag agtgtccct 660  
ctgtcgggaa tgccacatcc tcctctgccg gagaccagtc tggaagcca actgcctatg 720  
gggttattgc agctgctgcg gtgctcagtg caagcctggt caccgccacc ctccctctt 780  
tgtcctggct ccgagcccag gagegcctcc gccactggg gttactggtg gccatgaagg 840  
agtccctgct gctgtcagaa cagaagacct cgctgccctg aggacaagca cttgccacca 900  
ccgtcaactca gccctgggcg tagccggaca ggaggagagc agtgatgcgg atgggtaccc 960  
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agctaggatg gggaacctgc cacagccaga actgaggggc tggccccagg cagctcccag 1140  
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aagtgtcttc 1210

<210> 127  
<211> 282  
<212> PRT  
<213> Homo sapiens

<400> 127  
Met Ser Gly Gly Trp Met Ala Gln Val Gly Ala Trp Arg Thr Gly Ala  
1 5 10 15  
Leu Gly Leu Ala Leu Leu Leu Leu Leu Gly Leu Gly Leu Gly Leu Glu  
20 25 30  
Ala Ala Ala Ser Pro Leu Ser Thr Pro Thr Ser Ala Gln Ala Ala Gly  
35 40 45  
Pro Ser Ser Gly Ser Cys Pro Pro Thr Lys Phe Gln Cys Arg Thr Ser  
50 55 60  
Gly Leu Cys Val Pro Leu Thr Trp Arg Cys Asp Arg Asp Leu Asp Cys  
65 70 75 80

&lt;210&gt; 129

<211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 129  
 ttggttccac agccgagctc gtcg

24

<210> 130  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 130  
 gaggaggagt gcaggattga gccatgtacc cagaaagggc aatgcccacc

50

<210> 131  
 <211> 1843  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> modified\_base  
 <222> (1837)  
 <223> a, t, c or g

<400> 131  
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 cagactcttg caagctggat gccctctgtg gatgaaagat gtatcatgga atgaaccgga 180  
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 cgggcggggt cgatgacctt caagtgtgtg ctgaccccg cttcccgag aatggcttca 360  
 ggacccccag cggaggggtt ttctttgaag gctctgtagc ccgatttcac tgccaagacg 420  
 gattcaagct gaaggcgctt acaaagagac tgtgtttgaa gcattttaat ggaaccctag 480  
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 aagatgctga gattcataac aagacatata gacatggaga gaagctaate atcaattgtc 600  
 atgaaggatt caagatccgg taccccgacc tacacaatat ggtttcatta tgtcgcgatg 660  
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 agcaaacgtg gccacgaccc catgagaccc tcttgaccac gtggaagatt gtggcggtca 1140



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 gcttgagtgc cttaggcccc gggtagatgg cctctgtggg ccagggtgc cccttaccgc 1380  
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 ctcccaggtg ccaagagagc acccaaccctg cttcggacaa ccctgacata attgccagca 1560  
 cggcagagga ggtggcatcc accagcccag gcataccatca tgcccactgg gtgttggtcc 1620  
 taagaaactg attgattaaa aaatttccca aagtgtcctg aagtgtctct tcaaatacat 1680  
 gttgatctgt ggagttgatt cctttccttc tcttggtttt agacaaatgt aaacaaagct 1740  
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<210> 132

<211> 490

<212> PRT

<213> Homo sapiens

<400> 132

Met Tyr His Gly Met Asn Pro Ser Asn Gly Asp Gly Phe Leu Glu Gln  
 1 5 10 15

Gln Gln Gln Gln Gln Gln Pro Gln Ser Pro Gln Arg Leu Leu Ala Val  
 20 25 30

Ile Leu Trp Phe Gln Leu Ala Leu Cys Phe Gly Pro Ala Gln Leu Thr  
 35 40 45

Gly Gly Phe Asp Asp Leu Gln Val Cys Ala Asp Pro Gly Ile Pro Glu  
 50 55 60

Asn Gly Phe Arg Thr Pro Ser Gly Gly Val Phe Phe Glu Gly Ser Val  
 65 70 75 80

Ala Arg Phe His Cys Gln Asp Gly Phe Lys Leu Lys Gly Ala Thr Lys  
 85 90 95

Arg Leu Cys Leu Lys His Phe Asn Gly Thr Leu Gly Trp Ile Pro Ser  
 100 105 110

Asp Asn Ser Ile Cys Val Gln Glu Asp Cys Arg Ile Pro Gln Ile Glu  
 115 120 125

Asp Ala Glu Ile His Asn Lys Thr Tyr Arg His Gly Glu Lys Leu Ile  
 130 135 140

Ile Thr Cys His Glu Gly Phe Lys Ile Arg Tyr Pro Asp Leu His Asn  
 145 150 155 160

Met Val Ser Leu Cys Arg Asp Asp Gly Thr Trp Asn Asn Leu Pro Ile  
 165 170 175

Cys Gln Gly Cys Leu Arg Pro Leu Ala Ser Ser Asn Gly Tyr Val Asn

180	185	190
Ile Ser Glu Leu Gln Thr Ser Phe Pro Val Gly Thr Val Ile Ser Tyr		
195	200	205
Arg Cys Phe Pro Gly Phe Lys Leu Asp Gly Ser Ala Tyr Leu Glu Cys		
210	215	220
Leu Gln Asn Leu Ile Trp Ser Ser Ser Pro Pro Arg Cys Leu Ala Leu		
225	230	235 240
Glu Ala Gln Val Cys Pro Leu Pro Pro Met Val Ser His Gly Asp Phe		
	245	250 255
Val Cys His Pro Arg Pro Cys Glu Arg Tyr Asn His Gly Thr Val Val		
	260	265 270
Glu Phe Tyr Cys Asp Pro Gly Tyr Ser Leu Thr Ser Asp Tyr Lys Tyr		
	275	280 285
Ile Thr Cys Gln Tyr Gly Glu Trp Phe Pro Ser Tyr Gln Val Tyr Cys		
	290	295 300
Ile Lys Ser Glu Gln Thr Trp Pro Ser Thr His Glu Thr Leu Leu Thr		
305	310	315 320
Thr Trp Lys Ile Val Ala Phe Thr Ala Thr Ser Val Leu Leu Val Leu		
	325	330 335
Leu Leu Val Ile Leu Ala Arg Met Phe Gln Thr Lys Phe Lys Ala His		
	340	345 350
Phe Pro Pro Arg Gly Pro Pro Arg Ser Ser Ser Ser Asp Pro Asp Phe		
	355	360 365
Val Val Val Asp Gly Val Pro Val Met Leu Pro Ser Tyr Asp Glu Ala		
	370	375 380
Val Ser Gly Gly Leu Ser Ala Leu Gly Pro Gly Tyr Met Ala Ser Val		
385	390	395 400
Gly Gln Gly Cys Pro Leu Pro Val Asp Asp Gln Ser Pro Pro Ala Tyr		
	405	410 415
Pro Gly Ser Gly Asp Thr Asp Thr Gly Pro Gly Glu Ser Glu Thr Cys		
	420	425 430
Asp Ser Val Ser Gly Ser Ser Glu Leu Leu Gln Ser Leu Tyr Ser Pro		
	435	440 445
Pro Arg Cys Gln Glu Ser Thr His Pro Ala Ser Asp Asn Pro Asp Ile		
	450	455 460

Ile Ala Ser Thr Ala Glu Glu Val Ala Ser Thr Ser Pro Gly Ile His  
 465 470 475 480

His Ala His Trp Val Leu Phe Leu Arg Asn  
 485 490

<210> 133

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 133

atctcctatc gctgctttcc cgg

23

<210> 134

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 134

agccaggatc gcagtaaaac tcc

23

<210> 135

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 135

atttaaactt gatgggtctg cgtatcttga gtgcttaca aaccttatct

50

<210> 136

<211> 1815

<212> DNA

<213> Homo sapiens

<400> 136

cccacgcgtc cgctccgcgc cctccccccc gctcccgtg cggtcgctg gtggcctaga 60  
 gatgctgctg ccgcggttgc agttgtcgcg cagcctctg ccgcccagcc cgtccaccg 120  
 ccgtagcgcc cgagtgtcgg ggggcgcacc cgagtcgggc catgaggccg ggaaccgcgc 180  
 tacaggccgt gctgctggcc gtgctgctgg tggggtcgc ggccgcgacg ggtcgctgc 240  
 tgagtgcctc ggatttggac ctgagaggag ggcagccagt ctgccgggga gggacacaga 300

```

ggccttggtta taaagtcatt tacttccatg atacttctcg aagactgaac tttgaggaag 360
ccaaagaagc ctgcaggagg gatggaggcc agctagtcag catcgagtct gaagatgaac 420
agaaactgat agaaaagttc attgaaaacc tcttgccatc tgatgggtgac ttctggattg 480
ggctcaggag gcgtgaggag aaacaaagca atagcacagc ctgccaggac ctttatgctt 540
ggactgatgg cagcatatca caatttagga actggtatgt ggatgagccg tcctgcggca 600
gcgaggtctg cgtgggtcatg taccatcagc catcggcacc cgtgggcacg ggaggccctt 660
acatgttcca gtggaatgat gaccggtgca acatgaagaa caatttcatt tgcaaattt 720
ctgatgagaa accagcagtt ccttctagag aagctgaagg tgaggaaaca gagctgacaa 780
cacctgtact tccagaagaa acacaggaag aagatgccaa aaaaacattt aaagaaagta 840
gagaagctgc cttgaatctg gcctacatcc taatccccag cattccccctt ctctcctcc 900
ttgtgggtcac cacagttgta tgttgggttt ggatctgtag aaaaagaaaa cgggagcagc 960
cagaccctag cacaagaag caacacacca tctggccctc tctcaccag ggaaacagcc 1020
cggacctaga ggtctacaat gtcataagaa aacaaagcga agctgactta gctgagacc 1080
ggccagacct gaagaatatt tcattccgag tgtgttcggg agaagccact cccgatgaca 1140
tgtcttgtga ctatgacaac atggctgtga acccatcaga aagtgggttt gtgactctgg 1200
tgagcgtgga gagtggattt gtgaccaatg acatttatga gttctcccca gaccaaatgg 1260
ggaggagtaa ggagtctgga tgggtggaaa atgaaatata tggttattag gacatataaa 1320
aaactgaaac tgacaacaat ggaaaagaaa tgataagcaa aatcctctta tttctataa 1380
ggaaaatata cagaaggtct atgaacaagc ttagatcagg tcctgtggat gagcatgtgg 1440
tccccacgac ctctgtttgg acccccacgt tttggctgta tcctttatcc cagccagtca 1500
tccagctcga ccttatgaga aggtaccttg cccaggtctg gcacatagta gagtctcaat 1560
aaatgtcact tggttggttg tatctaactt ttaagggaca gagctttacc tggcagtgat 1620
aaagatgggc tgtggagctt ggaaaaccac ctctgttttc cttgctctat acagcagcac 1680
atattatcat acagacagaa aatccagaat cttttcaaag cccacatatg tagcacagc 1740
ttggcctgtg catcggcaat tctcatatct gtttttttca aagaataaaa tcaaataaag 1800
agcaggaaaa aaaaaa 1815

```

&lt;210&gt; 137

&lt;211&gt; 382

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 137

```

Met Arg Pro Gly Thr Ala Leu Gln Ala Val Leu Leu Ala Val Leu Leu
  1              5              10              15

```

```

Val Gly Leu Arg Ala Ala Thr Gly Arg Leu Leu Ser Ala Ser Asp Leu
      20              25              30

```

```

Asp Leu Arg Gly Gly Gln Pro Val Cys Arg Gly Gly Thr Gln Arg Pro
      35              40              45

```

```

Cys Tyr Lys Val Ile Tyr Phe His Asp Thr Ser Arg Arg Leu Asn Phe
      50              55              60

```

```

Glu Glu Ala Lys Glu Ala Cys Arg Arg Asp Gly Gly Gln Leu Val Ser
      65              70              75              80

```

```

Ile Glu Ser Glu Asp Glu Gln Lys Leu Ile Glu Lys Phe Ile Glu Asn
      85              90              95

```

```

Leu Leu Pro Ser Asp Gly Asp Phe Trp Ile Gly Leu Arg Arg Arg Glu
      100              105              110

```

Glu Lys Gln Ser Asn Ser Thr Ala Cys Gln Asp Leu Tyr Ala Trp Thr  
 115 120 125  
 Asp Gly Ser Ile Ser Gln Phe Arg Asn Trp Tyr Val Asp Glu Pro Ser  
 130 135 140  
 Cys Gly Ser Glu Val Cys Val Val Met Tyr His Gln Pro Ser Ala Pro  
 145 150 155 160  
 Ala Gly Ile Gly Gly Pro Tyr Met Phe Gln Trp Asn Asp Asp Arg Cys  
 165 170 175  
 Asn Met Lys Asn Asn Phe Ile Cys Lys Tyr Ser Asp Glu Lys Pro Ala  
 180 185 190  
 Val Pro Ser Arg Glu Ala Glu Gly Glu Glu Thr Glu Leu Thr Thr Pro  
 195 200 205  
 Val Leu Pro Glu Glu Thr Gln Glu Glu Asp Ala Lys Lys Thr Phe Lys  
 210 215 220  
 Glu Ser Arg Glu Ala Ala Leu Asn Leu Ala Tyr Ile Leu Ile Pro Ser  
 225 230 235 240  
 Ile Pro Leu Leu Leu Leu Val Val Thr Thr Val Val Cys Trp Val  
 245 250 255  
 Trp Ile Cys Arg Lys Arg Lys Arg Glu Gln Pro Asp Pro Ser Thr Lys  
 260 265 270  
 Lys Gln His Thr Ile Trp Pro Ser Pro His Gln Gly Asn Ser Pro Asp  
 275 280 285  
 Leu Glu Val Tyr Asn Val Ile Arg Lys Gln Ser Glu Ala Asp Leu Ala  
 290 295 300  
 Glu Thr Arg Pro Asp Leu Lys Asn Ile Ser Phe Arg Val Cys Ser Gly  
 305 310 315 320  
 Glu Ala Thr Pro Asp Asp Met Ser Cys Asp Tyr Asp Asn Met Ala Val  
 325 330 335  
 Asn Pro Ser Glu Ser Gly Phe Val Thr Leu Val Ser Val Glu Ser Gly  
 340 345 350  
 Phe Val Thr Asn Asp Ile Tyr Glu Phe Ser Pro Asp Gln Met Gly Arg  
 355 360 365  
 Ser Lys Glu Ser Gly Trp Val Glu Asn Glu Ile Tyr Gly Tyr  
 370 375 380

<211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 138  
 gttcattgaa aacctcttgc catctgatgg tgacttctgg attgggctca 50

<210> 139  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 139  
 aagccaaaga agcctgcagg aggg 24

<210> 140  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 140  
 cagtccaagc ataaagggtcc tggc 24

<210> 141  
 <211> 1514  
 <212> DNA  
 <213> Homo sapiens

<400> 141  
 ggggtctccc tcaggggcgg gaggcacagc ggtccctgct tgctgaaggg ctggatgtac 60  
 gcatccgcag gttcccgagg acttgggggc gcccgctgag ccccggcggc cgcagaagac 120  
 ttgtgtttgc ctctgcagc ctcaaccggg agggcagcga gggcctacca ccattgatcac 180  
 tgggtgtgttc agcatgcgt tgtggacccc agtgggcgtc ctgacctcgc tggcgactcg 240  
 cctgcaccag cggcggggtg ccctggccga gctgcaggag gccgatggcc agtgtccggg 300  
 cgaccgcagc ctgctgaagt tgaaaatggt gcaggctcgtg ttctgacacg gggctcggag 360  
 tctctctcaag ccgctcccgc tggaggagca ggtagagtgg aacccccagc tattagaggt 420  
 cccaccccaa actcagtttg attacacagt caccaatcta gctgggtggtc cgaaaccata 480  
 ttctccttac gactctcaat accatgagac caccctgaag gggggcatgt ttgctgggca 540  
 gctgaccaag gtgggcatgc agcaaagtgt tgccttggga gagagactga ggaagaacta 600  
 tgtggaagac attccctttc ttccaccaac cttcaaccca caggaggtct ttattcgttc 660  
 cactaacatt tttcggaatc tggagtcacac ccgttggttg ctggctgggc ttttccagtg 720

```

tcagaaagaa ggacccatca tcaccacac tgatgaagca gattcagaag tttgtatcc 780
caactaccaa agctgctgga gctgaggca gagaaccaga ggccggagga agactgcctc 840
tttacagcca ggaatctcag aggatttgaa aaaggtgaag gacaggatgg gcattgacag 900
tagtgataaa gtggacttct tcactctctt ggacaacgtg gctgccgagc aggcacacaa 960
cctcccaage tgcccatgc tgaagagatt tgcacggatg atcgaacaga gagctgtgga 1020
cacatccttg tacatactgc ccaaggaaga cagggaagt cttcagatgg cagtagggcc 1080
attcctccac atcctagaga gcaacctgtt gaaagccatg gactctgcca ctgcccccca 1140
caagatcaga aagctgtatc tctatgcggc tcatgatgtg accttcatac cgtctttaat 1200
gacctggggg atttttgacc acaaattggc accgtttgct gttgacctga ccatggaact 1260
ttaaccagcac ctggaatcta aggagtgggt tgtgcagctc tattaccacg ggaaggagca 1320
ggtgccgaga gggtgccttg atgggtcttg cccgtgggac atgttcttga atgccatgtc 1380
agtttatacc ttaagcccag aaaaatacca tgcactctgc tctcaaacctc aggtgatgga 1440
agttggaaat gaagagtaac tgatttataa aagcaggatg tgttgatttt aaaataaagt 1500
gcctttatac aatg 1514

```

&lt;210&gt; 142

&lt;211&gt; 428

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 142

```

Met Ile Thr Gly Val Phe Ser Met Arg Leu Trp Thr Pro Val Gly Val
  1                      5                      10                      15

```

```

Leu Thr Ser Leu Ala Tyr Cys Leu His Gln Arg Arg Val Ala Leu Ala
          20                      25                      30

```

```

Glu Leu Gln Glu Ala Asp Gly Gln Cys Pro Val Asp Arg Ser Leu Leu
          35                      40                      45

```

```

Lys Leu Lys Met Val Gln Val Val Phe Arg His Gly Ala Arg Ser Pro
          50                      55                      60

```

```

Leu Lys Pro Leu Pro Leu Glu Glu Gln Val Glu Trp Asn Pro Gln Leu
          65                      70                      75                      80

```

```

Leu Glu Val Pro Pro Gln Thr Gln Phe Asp Tyr Thr Val Thr Asn Leu
          85                      90                      95

```

```

Ala Gly Gly Pro Lys Pro Tyr Ser Pro Tyr Asp Ser Gln Tyr His Glu
          100                      105                      110

```

```

Thr Thr Leu Lys Gly Gly Met Phe Ala Gly Gln Leu Thr Lys Val Gly
          115                      120                      125

```

```

Met Gln Gln Met Phe Ala Leu Gly Glu Arg Leu Arg Lys Asn Tyr Val
          130                      135                      140

```

```

Glu Asp Ile Pro Phe Leu Ser Pro Thr Phe Asn Pro Gln Glu Val Phe
          145                      150                      155                      160

```

```

Ile Arg Ser Thr Asn Ile Phe Arg Asn Leu Glu Ser Thr Arg Cys Leu
          165                      170                      175

```

Leu Ala Gly Leu Phe Gln Cys Gln Lys Glu Gly Pro Ile Ile Ile His  
 180 185 190  
 Thr Asp Glu Ala Asp Ser Glu Val Leu Tyr Pro Asn Tyr Gln Ser Cys  
 195 200 205  
 Trp Ser Leu Arg Gln Arg Thr Arg Gly Arg Arg Gln Thr Ala Ser Leu  
 210 215 220  
 Gln Pro Gly Ile Ser Glu Asp Leu Lys Lys Val Lys Asp Arg Met Gly  
 225 230 235 240  
 Ile Asp Ser Ser Asp Lys Val Asp Phe Phe Ile Leu Leu Asp Asn Val  
 245 250 255  
 Ala Ala Glu Gln Ala His Asn Leu Pro Ser Cys Pro Met Leu Lys Arg  
 260 265 270  
 Phe Ala Arg Met Ile Glu Gln Arg Ala Val Asp Thr Ser Leu Tyr Ile  
 275 280 285  
 Leu Pro Lys Glu Asp Arg Glu Ser Leu Gln Met Ala Val Gly Pro Phe  
 290 295 300  
 Leu His Ile Leu Glu Ser Asn Leu Leu Lys Ala Met Asp Ser Ala Thr  
 305 310 315 320  
 Ala Pro Asp Lys Ile Arg Lys Leu Tyr Leu Tyr Ala Ala His Asp Val  
 325 330 335  
 Thr Phe Ile Pro Leu Leu Met Thr Leu Gly Ile Phe Asp His Lys Trp  
 340 345 350  
 Pro Pro Phe Ala Val Asp Leu Thr Met Glu Leu Tyr Gln His Leu Glu  
 355 360 365  
 Ser Lys Glu Trp Phe Val Gln Leu Tyr Tyr His Gly Lys Glu Gln Val  
 370 375 380  
 Pro Arg Gly Cys Pro Asp Gly Leu Cys Pro Leu Asp Met Phe Leu Asn  
 385 390 395 400  
 Ala Met Ser Val Tyr Thr Leu Ser Pro Glu Lys Tyr His Ala Leu Cys  
 405 410 415  
 Ser Gln Thr Gln Val Met Glu Val Gly Asn Glu Glu  
 420 425

&lt;210&gt; 143

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence



<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 143

ccaactacca aagctgctgg agcc

24

<210> 144

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 144

gcagctctat taccacggga agga

24

<210> 145

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 145

tctttcccggt ggtaatagag ctgc

24

<210> 146

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 146

ggcagagaac cagaggccgg aggagactgc ctctttacag ccagg

45

<210> 147

<211> 1686

<212> DNA

<213> Homo sapiens

<400> 147

ctctctttaa cataacttgca gctaaaacta aatattgctg cttggggacc tctttctagc 60  
cttaaatttc agctcatcac ctacacctgc cttgggtcatg gctctgctat tctccttgat 120  
ccttgccatt tgcaccagac ctggattcct agcgtctcca tctggagtgc ggctgggtggg 180

```

gggcctccac cgctgtgaag ggcggtgga ggtggaacag aaagggcagt ggggcaccgt 240
gtgtgatgac ggctgggaca ttaaggacgt ggctgtgttg tgccggggagc tgggctgtgg 300
agctgccagc ggaaccccta gtggtatatt gtatgagcca ccagcagaaa aagagcaaaa 360
ggctctcacc caatcagtcg gttgcacagg aacagaagat acattggctc agtgtgagca 420
agaagaagtt tatgattgtt cacatgatga agatgctggg gcacgtgtgt agaaccacaga 480
gagctctttc tccccagtc cagaggggtg caggctggct gacggccctg ggcattgcaa 540
gggacgcgtg gaagtgaagc accagaacca gtggtatacc gtgtgccaga caggctggag 600
cctccggggc gcaaagggtg tgtgccggca gctgggatgt gggagggctg tactgactca 660
aaaacgctgc aacaagcatg cctatggccg aaaacccatc tggttgagcc agatgtcatg 720
ctcaggacga gaagcaaccc ttcaggattg ccttctgagg ccttggggga agaacacctg 780
caaccatgat gaagacacgt gggtcgaatg tgaagatccc tttgacttga gactagtagg 840
aggagacaac ctctgctctg ggcgactgga ggtgctgcac aagggcgatg ggggctctgt 900
ctgtgatgac aactggggag aaaaggagga ccagggtgta tgcaagcaac tgggctgtgg 960
gaagtccttc tctccctcct tcagagaccg gaaatgctat ggcctggggg ttggccgcat 1020
ctggctggat aatgttcgtt gctcagggga ggagcagtc ctggagcagt gccagcacag 1080
attttggggg tttcacgact gcacccacca ggaagatgtg gctgtcatct gctcagtgtg 1140
ggtgggcac atctaactct ttgagtgcct gaatagaaga aaaacacaga agaagggagc 1200
atttactgtc tacatgactg catgggatga acactgatct tcttctgccc ttggactggg 1260
acttatactt ggtgcccctg attctcaggg cttcagagtt ggatcagaac ttacaacatc 1320
aggtctagtt ctcaggccat cagacatagt ttggaactac atcaccacct ttcctatgtc 1380
tcacattgc acacagcaga tcccagcct ccataattgt gtgtatcaac tacttaata 1440
cattctcaca cacacacaca cacacacaca cacacacaca cacacataca ccattgtcc 1500
tggttctctg aagaactctg acaaaatata gattttggta ctgaaagaga ttctagagga 1560
acggaatttt aaggataaat tttctgaatt ggttatggg tttctgaaat tggtctata 1620
atctaattag atataaaatt ctggttaact tatttacaat aataaagata gcactatgtg 1680
ttcaaa 1686

```

&lt;210&gt; 148

&lt;211&gt; 347

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 148

```

Met Ala Leu Leu Phe Ser Leu Ile Leu Ala Ile Cys Thr Arg Pro Gly
  1                      5                      10                      15

```

```

Phe Leu Ala Ser Pro Ser Gly Val Arg Leu Val Gly Gly Leu His Arg
      20                      25                      30

```

```

Cys Glu Gly Arg Val Glu Val Glu Gln Lys Gly Gln Trp Gly Thr Val
      35                      40                      45

```

```

Cys Asp Asp Gly Trp Asp Ile Lys Asp Val Ala Val Leu Cys Arg Glu
      50                      55                      60

```

```

Leu Gly Cys Gly Ala Ala Ser Gly Thr Pro Ser Gly Ile Leu Tyr Glu
      65                      70                      75                      80

```

```

Pro Pro Ala Glu Lys Glu Gln Lys Val Leu Ile Gln Ser Val Ser Cys
      85                      90                      95

```

```

Thr Gly Thr Glu Asp Thr Leu Ala Gln Cys Glu Gln Glu Glu Val Tyr
      100                      105                      110

```

Asp Cys Ser His Asp Glu Asp Ala Gly Ala Ser Cys Glu Asn Pro Glu  
 115 120 125

Ser Ser Phe Ser Pro Val Pro Glu Gly Val Arg Leu Ala Asp Gly Pro  
 130 135 140

Gly His Cys Lys Gly Arg Val Glu Val Lys His Gln Asn Gln Trp Tyr  
 145 150 155 160

Thr Val Cys Gln Thr Gly Trp Ser Leu Arg Ala Ala Lys Val Val Cys  
 165 170 175

Arg Gln Leu Gly Cys Gly Arg Ala Val Leu Thr Gln Lys Arg Cys Asn  
 180 185 190

Lys His Ala Tyr Gly Arg Lys Pro Ile Trp Leu Ser Gln Met Ser Cys  
 195 200 205

Ser Gly Arg Glu Ala Thr Leu Gln Asp Cys Pro Ser Gly Pro Trp Gly  
 210 215 220

Lys Asn Thr Cys Asn His Asp Glu Asp Thr Trp Val Glu Cys Glu Asp  
 225 230 235 240

Pro Phe Asp Leu Arg Leu Val Gly Gly Asp Asn Leu Cys Ser Gly Arg  
 245 250 255

Leu Glu Val Leu His Lys Gly Val Trp Gly Ser Val Cys Asp Asp Asn  
 260 265 270

Trp Gly Glu Lys Glu Asp Gln Val Val Cys Lys Gln Leu Gly Cys Gly  
 275 280 285

Lys Ser Leu Ser Pro Ser Phe Arg Asp Arg Lys Cys Tyr Gly Pro Gly  
 290 295 300

Val Gly Arg Ile Trp Leu Asp Asn Val Arg Cys Ser Gly Glu Glu Gln  
 305 310 315 320

Ser Leu Glu Gln Cys Gln His Arg Phe Trp Gly Phe His Asp Cys Thr  
 325 330 335

His Gln Glu Asp Val Ala Val Ile Cys Ser Val  
 340 345

<210> 149

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

## oligonucleotide probe

<400> 149  
ttcagctcat caccttcacc tgcc 24

<210> 150  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 150  
ggctcatata aaataccact aggg 24

<210> 151  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 151  
gggcctccac cgctgtgaag ggcgggtgga ggtggaacag aaaggccagt 50

<210> 152  
<211> 1427  
<212> DNA  
<213> Homo sapiens

<400> 152  
actgcaactcg gttctatcga ttgaattccc cggggatcct ctagagatcc ctcgacctcg 60  
acccaecggt ccgcggacgc gtgggcggac gcgtgggccc gctaccagga agagtctgcc 120  
gaagggtgaag gccatggact tcatcacctc cacagccatc ctgcccctgc tgttcggctg 180  
cctgggcgctc ttccggcctct tccggctgct gcagtgggtg cgcgggaagg cctacctgcg 240  
gaatgctgtg gtggtgatca caggcgccac ctccaggctg ggcaaagaat gtgcaaaaagt 300  
cttctatgct gcgggtgcta aactggtgct ctgtggcccg aatggtgggg ccctagaaga 360  
gctcatcaga gaacttaccg cttctcatgc caccaagggtg cagacacaca agccttactt 420  
ggtgaccttc gacctcacag actctggggc catagtgtga gcagcagctg agatcctgca 480  
gtgctttggc tatgtcgaca tacttgtcaa caatgctggg atcagctacc gtggtaccat 540  
catggacacc acagtggatg tggacaagag ggtcatggag acaaactact ttggcccagt 600  
tgctctaacg aaagcactcc tgccctccat gatcaagagg aggcaaggcc acattgtcgc 660  
catcagcagc atccagggca agatgagcat tcccttttca tcagcatatg cagcctccaa 720  
gcacgcaacc caggctttct ttgaactgtc gcgtgccgag atggaacagt atgaaattga 780  
ggtgaccgtc atcagccccg gctacatcca caccacctc tctgtaaatg ccatcacccg 840  
ggatggatct aggtatggag ttatggacac caccacagcc cagggccgaa gccctgtgga 900  
ggtggcccag gatgttcttg ctgctgtggg gaagaagaag aaagatgtga tccctggctga 960  
cttactgcct tccctggctg tttatcttcg aactctggct cctgggctct tcttcagcct 1020  
catggcctcc agggccagaa aagagcggaa atccaagaac tccagtact ctgaccagcc 1080

```

agggccaggg cagagaagca gcactcttag gcttgcttac tctacaaggg acagttgcat 1140
ttgttgagac tttaatggag atttgtctca caagtgggaa agactgaaga aacacatctc 1200
gtgcagatct gctggcagag gacaatcaaa aacgacaaca agcttcttcc cagggtgagg 1250
ggaaacactt aaggaataaa tatggagctg gggtttaaca ctaaaaacta gaaataaaca 1320
tctcaaacag taaaaaaaaa aaaaaagggc ggccgcgact ctagagtcga cctgcagaag 1380
cttgcccgcc atggcccaac ttgtttattg cagcttataa tgggttac 1427

```

<210> 153

<211> 310

<212> PRT

<213> Homo sapiens

<400> 153

```

Met Asp Phe Ile Thr Ser Thr Ala Ile Leu Pro Leu Leu Phe Gly Cys
  1             5             10             15

```

```

Leu Gly Val Phe Gly Leu Phe Arg Leu Leu Gln Trp Val Arg Gly Lys
      20             25             30

```

```

Ala Tyr Leu Arg Asn Ala Val Val Val Ile Thr Gly Ala Thr Ser Gly
      35             40             45

```

```

Leu Gly Lys Glu Cys Ala Lys Val Phe Tyr Ala Ala Gly Ala Lys Leu
      50             55             60

```

```

Val Leu Cys Gly Arg Asn Gly Gly Ala Leu Glu Glu Leu Ile Arg Glu
      65             70             75             80

```

```

Leu Thr Ala Ser His Ala Thr Lys Val Gln Thr His Lys Pro Tyr Leu
      85             90             95

```

```

Val Thr Phe Asp Leu Thr Asp Ser Gly Ala Ile Val Ala Ala Ala Ala
      100            105            110

```

```

Glu Ile Leu Gln Cys Phe Gly Tyr Val Asp Ile Leu Val Asn Asn Ala
      115            120            125

```

```

Gly Ile Ser Tyr Arg Gly Thr Ile Met Asp Thr Thr Val Asp Val Asp
      130            135            140

```

```

Lys Arg Val Met Glu Thr Asn Tyr Phe Gly Pro Val Ala Leu Thr Lys
      145            150            155            160

```

```

Ala Leu Leu Pro Ser Met Ile Lys Arg Arg Gln Gly His Ile Val Ala
      165            170            175

```

```

Ile Ser Ser Ile Gln Gly Lys Met Ser Ile Pro Phe Arg Ser Ala Tyr
      180            185            190

```

```

Ala Ala Ser Lys His Ala Thr Gln Ala Phe Phe Asp Cys Leu Arg Ala
      195            200            205

```

```

Glu Met Glu Gln Tyr Glu Ile Glu Val Thr Val Ile Ser Pro Gly Tyr

```

210	215	220
Ile His Thr Asn Leu Ser Val Asn Ala Ile Thr Ala Asp Gly Ser Arg		
225	230	235 240
Tyr Gly Val Met Asp Thr Thr Thr Ala Gln Gly Arg Ser Pro Val Glu		
	245	250 255
Val Ala Gln Asp Val Leu Ala Ala Val Gly Lys Lys Lys Lys Asp Val		
	260	265 270
Ile Leu Ala Asp Leu Leu Pro Ser Leu Ala Val Tyr Leu Arg Thr Leu		
	275	280 285
Ala Pro Gly Leu Phe Phe Ser Leu Met Ala Ser Arg Ala Arg Lys Glu		
	290	295 300
Arg Lys Ser Lys Asn Ser		
305	310	

<210> 154  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 154  
 ggtgctaaac tggctgctctg tggc

24

<210> 155  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 155  
 cagggcaaga tgagcattcc

20

<210> 156  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 156  
tcatactgtt ccatactcggc acgc

24

<210> 157  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 157  
aatggtgggg cccatagaaga gctcatcaga gaactcaccg cttctcatgc

50

<210> 158  
<211> 1771  
<212> DNA  
<213> Homo sapiens

<400> 158  
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aaaaaaaaaa acacacccaaa cgctcgccagc cacaaaaggg atgaaatttc ttctggacat 120  
cctcctgctt cccccgttac tgatcgctcg ctccttagag tccttcgtga agctttttat 180  
tctaagagg agaaaatcag tcacccggga aatcgtgctg attacaggag ctgggcatgg 240  
aattggggaga ctgactgcct atgaatttgc taaacttaaa agcaagctgg ttctctggga 300  
tataaataag catggactgg aggaaacagc tgccaaatgc aagggaactgg gtgccaaggt 360  
tcataccttt gtggtagact gcagcaaccg agaagatatt tacagctctg caaagaaggt 420  
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acatttctgg actacaaaagg catttcttcc tgcaatgacg aagaataacc atggccatat 600  
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aagcaagttt gctgctgttg gatttcataa aactttgaca gatgaactgg ctgccttaca 720  
aataactgga gtcaaaaacaa catgtctgtg tctaatttc gtaaacactg gcttcatcaa 780  
aaatccaagt acaagtttgg gacccactct ggaacctgag gaagtggtaa acaggctgat 840  
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aacattggaa aggatccttc ctgagcggtt cctggcagtt ttaaaacgaa aaatcagttg 960  
taagtttgat gcagttattg gatataaaat gaaagcgcaa taagcaccta gttttctgaa 1020  
aactgattta ccaggtttag gttgatgtca tctaatagtg ccagaatttt aatgtttgaa 1080  
cttctgtttt ttctaattat cccattttct tcaatatcat ttttgaggct ttggcagttc 1140  
tcatttacta ccacttgttc tttagccaaa agctgattac atatgatata aacagagaaa 1200  
tacctttaga ggtgacttta aggaaaatga agaaaaagaa ccaaaatgac tttattaaaa 1260  
taattttcaa gattatttgt ggctcacctg aaggctttgc aaaatttgta ccataaccgt 1320  
ttatttaaca tatattttta tttttgattg cacttaaat ttgtataatt tgtgtttctt 1380  
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gccactctgt ttctgagag atacctcaca ttccaatgcc aaacatttct gcacagggaa 1560  
gctagagggtg gatacacgtg ttgcaagtat aaaagcatca ctgggattta aggagaattg 1620  
agagaatgta cccacaaatg gcagcaataa taaatggatc acacttaaaa aaaaaaaaaa 1680  
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1740  
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa a a 1771

<210> 159

<211> 300  
 <212> PRT  
 <213> Homo sapiens

<400> 159

Met	Lys	Phe	Leu	Leu	Asp	Ile	Leu	Leu	Leu	Leu	Pro	Leu	Leu	Ile	Val
1				5					10					15	
Cys	Ser	Leu	Glu	Ser	Phe	Val	Lys	Leu	Phe	Ile	Pro	Lys	Arg	Arg	Lys
		20					25						30		
Ser	Val	Thr	Gly	Glu	Ile	Val	Leu	Ile	Thr	Gly	Ala	Gly	His	Gly	Ile
	35						40					45			
Gly	Arg	Leu	Thr	Ala	Tyr	Glu	Phe	Ala	Lys	Leu	Lys	Ser	Lys	Leu	Val
	50					55					60				
Leu	Trp	Asp	Ile	Asn	Lys	His	Gly	Leu	Glu	Glu	Thr	Ala	Ala	Lys	Cys
65					70					75					80
Lys	Gly	Leu	Gly	Ala	Lys	Val	His	Thr	Phe	Val	Val	Asp	Cys	Ser	Asn
				85					90					95	
Arg	Glu	Asp	Ile	Tyr	Ser	Ser	Ala	Lys	Lys	Val	Lys	Ala	Glu	Ile	Gly
			100					105					110		
Asp	Val	Ser	Ile	Leu	Val	Asn	Asn	Ala	Gly	Val	Val	Tyr	Thr	Ser	Asp
	115						120					125			
Leu	Phe	Ala	Thr	Gln	Asp	Pro	Gln	Ile	Glu	Lys	Thr	Phe	Glu	Val	Asn
130						135					140				
Val	Leu	Ala	His	Phe	Trp	Thr	Thr	Lys	Ala	Phe	Leu	Pro	Ala	Met	Thr
145					150					155					160
Lys	Asn	Asn	His	Gly	His	Ile	Val	Thr	Val	Ala	Ser	Ala	Ala	Gly	His
			165						170					175	
Val	Ser	Val	Pro	Phe	Leu	Leu	Ala	Tyr	Cys	Ser	Ser	Lys	Phe	Ala	Ala
		180						185					190		
Val	Gly	Phe	His	Lys	Thr	Leu	Thr	Asp	Glu	Leu	Ala	Ala	Leu	Gln	Ile
	195						200					205			
Thr	Gly	Val	Lys	Thr	Thr	Cys	Leu	Cys	Pro	Asn	Phe	Val	Asn	Thr	Gly
	210					215					220				
Phe	Ile	Lys	Asn	Pro	Ser	Thr	Ser	Leu	Gly	Pro	Thr	Leu	Glu	Pro	Glu
225					230					235					240
Glu	Val	Val	Asn	Arg	Leu	Met	His	Gly	Ile	Leu	Thr	Glu	Gln	Lys	Met
			245						250					255	



Ile Phe Ile Pro Ser Ser Ile Ala Phe Leu Thr Thr Leu Glu Arg Ile  
                   260                                  265                                  270

Leu Pro Glu Arg Phe Leu Ala Val Leu Lys Arg Lys Ile Ser Val Lys  
                   275                                  280                                  285

Phe Asp Ala Val Ile Gly Tyr Lys Met Lys Ala Gln  
                   290                                  295                                  300

<210> 160

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
                   oligonucleotide probe

<400> 160

ggtgaaggca gaaattggag atg

23

<210> 161

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
                   oligonucleotide probe

<400> 161

atcccatgca tcagcctggt tacc

24

<210> 162

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
                   oligonucleotide probe

<400> 162

gctggtgtag tctatacatc agatttggtt gctacacaag atcctcag

48

<210> 163

<211> 2076

<212> DNA

<213> Homo sapiens

<400> 163

cccacggtc cgcggacgcg tgggtcgact agttctagat cgcgagcggc cgcccgcggc 60  
 tcagggagga gcaccgactg cgcgcaccc tgagagatgg ttggtgccat gtggaagggtg 120

```

attgtttcgc tggctcctggt gatgcctggc cccgtgtgatg ggctgtttcg ctccctatac 180
agaagtgttt ccattgccacc taagggagac tcaggacagc cattatttct cacccttac 240
attgaagctg ggaagatcca aaaaggaaga gaattgagtt tggctcgccc tttcccagga 300
ctgaacatga agagtttatgc cggcttcctc accgtgaata agacttaca cagcaacctc 360
ttcttctggt tcttcccagc tcagatacag ccagaagatg cccagtagt tctctggcta 420
caggggtggc cgggaggttc atccatgttt ggactctttg tggaaacatg gccttatggt 480
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caggaataca agaaggcaga aaaaaaagt tggaaagatc ttaaactctga cagtgaagtg 1380
gctgggttaca tccggcaagc gggtgacttc catcaggtaa ttattcgagg tggaggacat 1440
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gtgtttggaa atattattgg ataagaatag ctcaattatc ccaataaat ggatgaagct 1980
ataatagttt tggggaaaag attctcaaat gtataaagtc ttagaacaaa agaattcttt 2040
gaaataaaaa tattatatat aaaagtaaaa aaaaaa 2076

```

&lt;210&gt; 164

&lt;211&gt; 476

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 164

```

Met Val Gly Ala Met Trp Lys Val Ile Val Ser Leu Val Leu Leu Met
  1              5              10              15

```

```

Pro Gly Pro Cys Asp Gly Leu Phe Arg Ser Leu Tyr Arg Ser Val Ser
      20              25              30

```

```

Met Pro Pro Lys Gly Asp Ser Gly Gln Pro Leu Phe Leu Thr Pro Tyr
      35              40              45

```

```

Ile Glu Ala Gly Lys Ile Gln Lys Gly Arg Glu Leu Ser Leu Val Gly
      50              55              60

```

```

Pro Phe Pro Gly Leu Asn Met Lys Ser Tyr Ala Gly Phe Leu Thr Val

```

65		70		75		80
Asn Lys Thr Tyr	Asn Ser Asn Leu Phe	Phe Trp Phe Phe	Pro Ala Gln			
	85	90	95			
Ile Gln Pro Glu Asp	Ala Pro Val Val	Leu Trp Leu Gln	Gly Gly Pro			
	100	105	110			
Gly Gly Ser Ser Met	Phe Gly Leu Phe	Val Glu His Gly	Pro Tyr Val			
	115	120	125			
Val Thr Ser Asn Met	Thr Leu Arg Asp	Arg Asp Phe	Pro Trp Thr Thr			
	130	135	140			
Thr Leu Ser Met Leu	Tyr Ile Asp Asn	Pro Val Gly Thr	Gly Phe Ser			
	145	150	155	160		
Phe Thr Asp Asp Thr	His Gly Tyr Ala	Val Asn Glu Asp	Asp Val Ala			
	165	170	175			
Arg Asp Leu Tyr Ser	Ala Leu Ile Gln	Phe Phe Gln Ile	Phe Pro Glu			
	180	185	190			
Tyr Lys Asn Asn Asp	Phe Tyr Val Thr	Gly Glu Ser Tyr	Ala Gly Lys			
	195	200	205			
Tyr Val Pro Ala Ile	Ala His Leu Ile	His Ser Leu Asn	Pro Val Arg			
	210	215	220			
Glu Val Lys Ile Asn	Leu Asn Gly Ile	Ala Ile Gly Asp	Gly Tyr Ser			
	225	230	235	240		
Asp Pro Glu Ser Ile	Ile Gly Gly Tyr	Ala Glu Phe Leu	Tyr Gln Ile			
	245	250	255			
Gly Leu Leu Asp Glu	Lys Gln Lys Lys	Tyr Phe Gln Lys	Gln Cys His			
	260	265	270			
Glu Cys Ile Glu His	Ile Arg Lys Gln	Asn Trp Phe Glu	Ala Phe Glu			
	275	280	285			
Ile Leu Asp Lys Leu	Leu Asp Gly Asp	Leu Thr Ser Asp	Pro Ser Tyr			
	290	295	300			
Phe Gln Asn Val Thr	Gly Cys Ser Asn	Tyr Tyr Asn Phe	Leu Arg Cys			
	305	310	315	320		
Thr Glu Pro Glu Asp	Gln Leu Tyr Tyr	Val Lys Phe Leu	Ser Leu Pro			
	325	330	335			
Glu Val Arg Gln Ala	Ile His Val Gly	Asn Gln Thr Phe	Asn Asp Gly			
	340	345	350			

Thr Ile Val Glu Lys Tyr Leu Arg Glu Asp Thr Val Gln Ser Val Lys  
 355 360 365

Pro Trp Leu Thr Glu Ile Met Asn Asn Tyr Lys Val Leu Ile Tyr Asn  
 370 375 380

Gly Gln Leu Asp Ile Ile Val Ala Ala Ala Leu Thr Glu Arg Ser Leu  
 385 390 395 400

Met Gly Met Asp Trp Lys Gly Ser Gln Glu Tyr Lys Lys Ala Glu Lys  
 405 410 415

Lys Val Trp Lys Ile Phe Lys Ser Asp Ser Glu Val Ala Gly Tyr Ile  
 420 425 430

Arg Gln Ala Gly Asp Phe His Gln Val Ile Ile Arg Gly Gly Gly His  
 435 440 445

Ile Leu Pro Tyr Asp Gln Pro Leu Arg Ala Phe Asp Met Ile Asn Arg  
 450 455 460

Phe Ile Tyr Gly Lys Gly Trp Asp Pro Tyr Val Gly  
 465 470 475

<210> 165

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 165

ttccatgcca cctaagggag actc

24

<210> 166

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 166

tgcatgaggt gtgcaatggc tggc

24

<210> 167

<211> 24

<212> DNA

<213> Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 167

agctctcaga ggctggatcat aggg

24

&lt;210&gt; 168

&lt;211&gt; 50

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 168

gtcggccctt tcccaggact gaacatgaag agttatgccg gcttctctac

50

&lt;210&gt; 169

&lt;211&gt; 2477

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 169

```

cgagggcttt tccggctccg gaatggcaca tgtgggaatc ccagtcttgt tggctacaac 60
atttttccct ttctaacaa gttctaacag ctgttctaac agctagtgat caggggttct 120
tcttgctgga gaagaaagg ctgagggcag agcagggcac tctcactcag ggtgaccagc 180
tccttgcttc tctgtggata acagagcatg agaaagtga gagatgcagc ggagtgaggt 240
gatggaagtc taaaatagga aggaattttg tgtgcaatat cagactctgg gagcagttga 300
cctggagagc ctgggggagg gctgcctaa caagctttca aaaaacagga gcgacttcca 360
ctgggctggg ataagacgtg ccggtaggat agggaagact gggtttagtc ctaatatcaa 420
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tatagcataa aggctagaga ccaaaataga taacaggatt ccctgaacat tcctaagagg 600
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```

```

aaggatgacc ccaagttcca ctcatacgtg tccctgacct tcggtgcac ccgggccggg 1740
gtggaatacc gcctcctgca ggctgcttac ctggccaagc ctggggactc actggcccag 1800
gccttcaata tcaccagcca ggacgatgta ctctttgcca tcttctccaa agggcagaag 1860
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gtaaggaatg caagcgatt tcaatatttc ccaaacttta agaaaaaact ttaagaaggt 2460
acatctgcaa aagcaaa 2477

```

&lt;210&gt; 170

&lt;211&gt; 552

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 170

```

Met Gly Thr Leu Gly Gln Ala Ser Leu Phe Ala Pro Pro Gly Asn Tyr
  1              5              10              15

Phe Trp Ser Asp His Ser Ala Leu Cys Phe Ala Glu Ser Cys Glu Gly
      20              25              30

Gln Pro Gly Lys Val Glu Gln Met Ser Thr His Arg Ser Arg Leu Leu
      35              40              45

Thr Ala Ala Pro Leu Ser Met Glu Gln Arg Gln Pro Trp Pro Arg Ala
      50              55              60

Leu Glu Val Asp Ser Arg Ser Val Val Leu Leu Ser Val Val Trp Val
      65              70              75              80

Leu Leu Ala Pro Pro Ala Ala Gly Met Pro Gln Phe Ser Thr Phe His
      85              90              95

Ser Glu Asn Arg Asp Trp Thr Phe Asn His Leu Thr Val His Gln Gly
      100              105              110

Thr Gly Ala Val Tyr Val Gly Ala Ile Asn Arg Val Tyr Lys Leu Thr
      115              120              125

Gly Asn Leu Thr Ile Gln Val Ala His Lys Thr Gly Pro Glu Glu Asp
      130              135              140

Asn Lys Ser Arg Tyr Pro Pro Leu Ile Val Gln Pro Cys Ser Glu Val
      145              150              155              160

Leu Thr Leu Thr Asn Asn Val Asn Lys Leu Leu Ile Ile Asp Tyr Ser
      165              170              175

```

Glu Asn Arg Leu Leu Ala Cys Gly Ser Leu Tyr Gln Gly Val Cys Lys  
 180 185 190  
 Leu Leu Arg Leu Asp Asp Leu Phe Ile Leu Val Glu Pro Ser His Lys  
 195 200 205  
 Lys Glu His Tyr Leu Ser Ser Val Asn Lys Thr Gly Thr Met Tyr Gly  
 210 215 220  
 Val Ile Val Arg Ser Glu Gly Glu Asp Gly Lys Leu Phe Ile Gly Thr  
 225 230 235 240  
 Ala Val Asp Gly Lys Gln Asp Tyr Phe Pro Thr Leu Ser Ser Arg Lys  
 245 250 255  
 Leu Pro Arg Asp Pro Glu Ser Ser Ala Met Leu Asp Tyr Glu Leu His  
 260 265 270  
 Ser Asp Phe Val Ser Ser Leu Ile Lys Ile Pro Ser Asp Thr Leu Ala  
 275 280 285  
 Leu Val Ser His Phe Asp Ile Phe Tyr Ile Tyr Gly Phe Ala Ser Gly  
 290 295 300  
 Gly Phe Val Tyr Phe Leu Thr Val Gln Pro Glu Thr Pro Glu Gly Val  
 305 310 315 320  
 Ala Ile Asn Ser Ala Gly Asp Leu Phe Tyr Thr Ser Arg Ile Val Arg  
 325 330 335  
 Leu Cys Lys Asp Asp Pro Lys Phe His Ser Tyr Val Ser Leu Pro Phe  
 340 345 350  
 Gly Cys Thr Arg Ala Gly Val Glu Tyr Arg Leu Leu Gln Ala Ala Tyr  
 355 360 365  
 Leu Ala Lys Pro Gly Asp Ser Leu Ala Gln Ala Phe Asn Ile Thr Ser  
 370 375 380  
 Gln Asp Asp Val Leu Phe Ala Ile Phe Ser Lys Gly Gln Lys Gln Tyr  
 385 390 395 400  
 His His Pro Pro Asp Asp Ser Ala Leu Cys Ala Phe Pro Ile Arg Ala  
 405 410 415  
 Ile Asn Leu Gln Ile Lys Glu Arg Leu Gln Ser Cys Tyr Gln Gly Glu  
 420 425 430  
 Gly Asn Leu Glu Leu Asn Trp Leu Leu Gly Lys Asp Val Gln Cys Thr  
 435 440 445  
 Lys Ala Pro Val Pro Ile Asp Asp Asn Phe Cys Gly Leu Asp Ile Asn

450		455		460
Gln Pro Leu Gly Gly Ser Thr Pro Val Glu Gly Leu Thr Leu Tyr Thr				
465		470		480
Thr Ser Arg Asp Arg Met Thr Ser Val Ala Ser Tyr Val Tyr Asn Gly				
	485		490	495
Tyr Ser Val Val Phe Val Gly Thr Lys Ser Gly Lys Leu Lys Lys Val				
	500		505	510
Arg Val Tyr Glu Phe Arg Cys Ser Asn Ala Ile His Leu Leu Ser Lys				
	515		520	525
Glu Ser Leu Leu Glu Gly Ser Tyr Trp Trp Arg Phe Asn Tyr Arg Gln				
	530		535	540
Leu Tyr Phe Leu Gly Glu Gln Arg				
545		550		

&lt;210&gt; 171

&lt;211&gt; 20

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 171

tggaataaccg cctcctgcag

20

&lt;210&gt; 172

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 172

cttctgccct ttggagaaga tggc

24

&lt;210&gt; 173

&lt;211&gt; 43

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe



<400> 173  
ggactcaactg gccagggcct tcaatatcac cagccaggac gat

42

<210> 174  
<211> 3106  
<212> DNA  
<213> Homo sapiens

<220>  
<221> modified\_base  
<222> (1683)  
<223> a, t, c or g

<400> 174  
aggctcccgc gcgcggctga gtgcggactg gagtgggaac ccgggtcccc gcgcttagag 60  
aacacgcgat gaccacgtgg agcctccggc ggaggccggc ccgcacgctg ggactcctgc 120  
tgctggctcgt cttgggcttc ctgggtctcc gcaggctgga ctggagcacc ctggctccctc 180  
tgccgctccg ccacgcacag ctggggctgc agggccaagg ctggaacttc atgctggagg 240  
attccacctt ctggatcttc gggggctcca tccactattt ccgtgtgccc agggagtact 300  
ggagggaccg cctgctgaag atgaaggcct gtggcttgaa caccctcacc acctatgttc 360  
cgtggaacct gcatgagcca gaaagaggca aatttgactt ctctgggaac ctggacctgg 420  
aggccttcgt cctgatggcc gcagagatcg ggctgtgggt gattctgcgt ccaggccctc 480  
acatctgcag tgagatggac ctccggggct tggccagctg gctactccaa gacctggca 540  
tgaggctgag gacaacttac aagggttca ccgaagcagt ggacctttat ttgaccacc 600  
tgatgtccag ggtggtgcca ctccagtaca agcgtggggg acctatcatt gccgtgcagg 660  
tggaagaatga atatggttcc tataataaag accccgcata catgccctac gtcaagaagg 720  
cactggagga ccgtggcatt gtggaactgc tctgacttcc agacaacaag gatgggctga 780  
gcaaggggat tgtccaggga gtcttgacca ccacacttca gcaagcactc caccagctgc 840  
agctactgac cacccttctc ttcaacgtcc aggggactca gcccaagatg gtgatggagt 900  
actggacggg gtggtttgac tcgtggggag gccctcaca tatcttggat tcttctgagg 960  
ttttgaaaac cgtgtctgcc caactttggc ttcatgaatg gagccatgca ctccatgac tacaagtcag 1080  
acggaggcac caactttggc ttcatgaatg gagccatgca ctccatgac tacaagtcag 1140  
atgtcaccag ctatgactat gatgctgtgc tgacagaagc cggcgattac acggccaagt 1200  
acatgaagct tcgagacttc ttccgctcca tctcaggcat cctctccct cccccacctg 1260  
accttcttcc caagatgccg tatgagccct taacgccagt cttgtacctg tctctgtggg 1320  
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tgccagtcaa tgggggaaat ggacagtcc tccgggtacat tctctatgag accagcatca 1440  
cctcgtctgg catcctcagt ggccacgtgc atgatcgggg gcagggtgtt gtgaacacag 1500  
tatccatagg attcttggac tacaagacaa cgaagattgc tgtccccctg atccagggtt 1560  
acaccgtgct gaggatcttg gtggagaatc gtgggcgagt caactatggg gagaatattg 1620  
atgaccagcg caaaggetta attggaatc tctatctgaa tgattcacc ctgaaaaact 1680  
tcagaatcta tagcctggat atgaagaaga gcttctttca gaggttcggc ctggacaaat 1740  
ggngttccct cccagaaaca cccacattac ctgctttctt cttgggttagc ttgtccatca 1800  
gtccacgcgc ttgtgacacc tttctgaagc tggagggtcg ggagaagggg gttgtattca 1860  
tcaattggcca gaaccttgga cgttactgga acattggacc ccagaagacg ctttacctcc 1920  
caggtccctg gttgagcagc ggaatcaacc aggtcatcgt ttttgaggag acgatggcgg 1980  
gccctgcatt acagttcacg gaaaccccc acctgggcag gaaccagtac attaagttag 2040  
cgggtggcacc cctcctgct ggtgccagt ggagactgcc gcctcctctt gacctgaagc 2100  
ctggtggctg ctgccccacc cctcactgca aaagcatctc cttaagtagc aacctcaggg 2160  
actgggggct acagtctgcc cctgtctcag ctcaaaaccc taagcctgca gggaaagggt 2220  
ggatggctct gggcctggct ttgttgatga tggctttcct acagccctgc tcttgtgccg 2280  
aggctgtcgg gctgtctcta ggggtgggag agctaactag atcgcccagc ctttggccct

```

cagaaaaagt gctgaaacgt gcccttgcac cggacgtcac agccctgcga gcattctgctg 2340
gactcaggcg tgctctttgc tggttcctgg gaggttggc cacatccctc atggcccat 2400
tttatccccg aaatcctggg tgtgtcacca gtgtagaggg tggggaaggg gtgtctcacc 2460
tgagctgact ttgttcttcc ttcacaacct tctgagcctt ctttgggatt ctggaaggaa 2520
ctcggcgtga gaaacatgtg acttcccctt tcccttccca ctgctgctt cccacagggg 2580
gacaggctgg gctggagaaa cagaaatcct caccctgcgt cttcccaagt tagcaggtgt 2640
ctctggtggt cagtgaggag gacatgtgag tcctggcaga agccatggcc catgtctgca 2700
catccaggga ggaggacaga aggccagct cacatgtgag tcctggcaga agccatggcc 2760
catgtctgca catccaggga ggaggacaga aggccagct cacatgtgag tcctggcaga 2820
agccatggcc catgtctgca catccaggga ggaggacaga aggccagct cacatgtgag 2880
tcctggcaga agccatggcc catgtctgca catccaggga ggaggacaga aggccagct 2940
cagtggcccc cgctccccac cccccacgcc cgaacagcag gggcagagca gccctccttc 3000
gaagtgtgtc caagtccgca tttgagcctt gttctggggc ccagcccaac acctggcttg 3060
ggctcactgt cctgagttgc agtaaagcta taaccttgaa tcacaa

```

&lt;210&gt; 175

&lt;211&gt; 636

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; MOD\_RES

&lt;222&gt; (539)

&lt;223&gt; Any amino acid

&lt;400&gt; 175

```

Met Thr Thr Trp Ser Leu Arg Arg Arg Pro Ala Arg Thr Leu Gly Leu
  1             5             10             15

```

```

Leu Leu Leu Val Val Leu Gly Phe Leu Val Leu Arg Arg Leu Asp Trp
          20             25             30

```

```

Ser Thr Leu Val Pro Leu Arg Leu Arg His Arg Gln Leu Gly Leu Gln
      35             40             45

```

```

Ala Lys Gly Trp Asn Phe Met Leu Glu Asp Ser Thr Phe Trp Ile Phe
      50             55             60

```

```

Gly Gly Ser Ile His Tyr Phe Arg Val Pro Arg Glu Tyr Trp Arg Asp
      65             70             75             80

```

```

Arg Leu Leu Lys Met Lys Ala Cys Gly Leu Asn Thr Leu Thr Thr Tyr
          85             90             95

```

```

Val Pro Trp Asn Leu His Glu Pro Glu Arg Gly Lys Phe Asp Phe Ser
      100             105             110

```

```

Gly Asn Leu Asp Leu Glu Ala Phe Val Leu Met Ala Ala Glu Ile Gly
      115             120             125

```

```

Leu Trp Val Ile Leu Arg Pro Gly Pro Tyr Ile Cys Ser Glu Met Asp
      130             135             140

```

Leu Gly Gly Leu Pro Ser Trp Leu Leu Gln Asp Pro Gly Met Arg Leu  
 145 150 155 160

Arg Thr Thr Tyr Lys Gly Phe Thr Glu Ala Val Asp Leu Tyr Phe Asp  
 165 170 175

His Leu Met Ser Arg Val Val Pro Leu Gln Tyr Lys Arg Gly Gly Pro  
 180 185 190

Ile Ile Ala Val Gln Val Glu Asn Glu Tyr Gly Ser Tyr Asn Lys Asp  
 195 200 205

Pro Ala Tyr Met Pro Tyr Val Lys Lys Ala Leu Glu Asp Arg Gly Ile  
 210 215 220

Val Glu Leu Leu Leu Thr Ser Asp Asn Lys Asp Gly Leu Ser Lys Gly  
 225 230 235 240

Ile Val Gln Gly Val Leu Ala Thr Ile Asn Leu Gln Ser Thr His Glu  
 245 250 255

Leu Gln Leu Leu Thr Thr Phe Leu Phe Asn Val Gln Gly Thr Gln Pro  
 260 265 270

Lys Met Val Met Glu Tyr Trp Thr Gly Trp Phe Asp Ser Trp Gly Gly  
 275 280 285

Pro His Asn Ile Leu Asp Ser Ser Glu Val Leu Lys Thr Val Ser Ala  
 290 295 300

Ile Val Asp Ala Gly Ser Ser Ile Asn Leu Tyr Met Phe His Gly Gly  
 305 310 315 320

Thr Asn Phe Gly Phe Met Asn Gly Ala Met His Phe His Asp Tyr Lys  
 325 330 335

Ser Asp Val Thr Ser Tyr Asp Tyr Asp Ala Val Leu Thr Glu Ala Gly  
 340 345 350

Asp Tyr Thr Ala Lys Tyr Met Lys Leu Arg Asp Phe Phe Gly Ser Ile  
 355 360 365

Ser Gly Ile Pro Leu Pro Pro Pro Pro Asp Leu Leu Pro Lys Met Pro  
 370 375 380

Tyr Glu Pro Leu Thr Pro Val Leu Tyr Leu Ser Leu Trp Asp Ala Leu  
 385 390 395 400

Lys Tyr Leu Gly Glu Pro Ile Lys Ser Glu Lys Pro Ile Asn Met Glu  
 405 410 415

Asn Leu Pro Val Asn Gly Gly Asn Gly Gln Ser Phe Gly Tyr Ile Leu  
 420 425 430

Tyr Glu Thr Ser Ile Thr Ser Ser Gly Ile Leu Ser Gly His Val His  
 435 440 445

Asp Arg Gly Gln Val Phe Val Asn Thr Val Ser Ile Gly Phe Leu Asp  
 450 455 460

Tyr Lys Thr Thr Lys Ile Ala Val Pro Leu Ile Gln Gly Tyr Thr Val  
 465 470 475 480

Leu Arg Ile Leu Val Glu Asn Arg Gly Arg Val Asn Tyr Gly Glu Asn  
 485 490 495

Ile Asp Asp Gln Arg Lys Gly Leu Ile Gly Asn Leu Tyr Leu Asn Asp  
 500 505 510

Ser Pro Leu Lys Asn Phe Arg Ile Tyr Ser Leu Asp Met Lys Lys Ser  
 515 520 525

Phe Phe Gln Arg Phe Gly Leu Asp Lys Trp Xaa Ser Leu Pro Glu Thr  
 530 535 540

Pro Thr Leu Pro Ala Phe Phe Leu Gly Ser Leu Ser Ile Ser Ser Thr  
 545 550 555 560

Pro Cys Asp Thr Phe Leu Lys Leu Glu Gly Trp Glu Lys Gly Val Val  
 565 570 575

Phe Ile Asn Gly Gln Asn Leu Gly Arg Tyr Trp Asn Ile Gly Pro Gln  
 580 585 590

Lys Thr Leu Tyr Leu Pro Gly Pro Trp Leu Ser Ser Gly Ile Asn Gln  
 595 600 605

Val Ile Val Phe Glu Glu Thr Met Ala Gly Pro Ala Leu Gln Phe Thr  
 610 615 620

Glu Thr Pro His Leu Gly Arg Asn Gln Tyr Ile Lys  
 625 630 635

<210> 176

<211> 2505

<212> DNA

<213> Homo sapiens

<400> 176

ggggacgcgg agctgagagg ctccgggcta gctaggtgta ggggtggacg ggtcccagga 60  
 ccctggtgag ggttctctac ttggccttcg gtgggggtca agacgcaggc acctacgcca 120  
 aaggggagca aagccgggct cggcccagag cccccaggac ctccatctcc caatggtgga 180  
 ggaatccgac acgtgacggt ctgtccgccg tctcagacta gaggagcgt gtaaaccgcca 240  
 tggctcccaa gaagctgtcc tgccttcgtt ccctgctgct gccgctcagc ctgacgctac 300  
 tgctgccccca ggcagacact cggtcgttcg tagtgatag gggtcatgac cggtttctcc 360  
 tagacgggggc cccgttcgcg tatgtgtctg gcagcctgca ctactttcgg gtaccgcggg 420

```

tgcctttgggc cgaccggcctt ttgaagatgc gatggagcgg cctcaacgcc atacagtttt 480
atgtgccctg gaactaccac gagccacagc ctggggtcta taactttaat ggcagccggg 540
acctcattgc ctttctgaat gaggcagctc tagcgaacct gttggtcata ctgagaccag 600
gacettacat ctgtgcagag tgggagatgg ggggtctccc atcctggttg cttcgaaaac 660
ctgaaattca tctaagaacc tcagatccag acttccttgc cgcagtggac tcttggttca 720
aggtcttget gcccaagata tatccatggc tttatcacia tgggggcaac atcattagca 780
ttcaggtgga gaatgaatat ggtagctaca gagcctgtga cttcagctac atgaggcact 840
tggtctgggt cttccgtgca ctgctaggag aaaagatctt gctcttcacc acagatgggc 900
ctgaaggact caagtgtggc tccctccggg gactctatac cactgtagat tttggcccag 960
ctgacaacat gacccaaatc tttaccctgc ttcggaagta tgaaccccat gggccatttg 1020
taaactctga gtactacaca ggctggctgg attactgggg ccagaatcac tccacacggt 1080
ctgtgtcagc tgtaacccaa ggactagaga acatgctcaa gttgggagcc agtgtgaaca 1140
tgtacatggt ccatggaggt accaactttg gatattggaa tgggtgccgat aagaagggag 1200
gcttccttcc gattactacc agctatgact atgatgcacc tatactgaa gcaggggacc 1260
ccacacctaa gcttttttgc cttcgagatg tcatcagcaa gttccaggaa gttcctttgg 1320
gacctttacc tcccccgagc cccaagatga tgcctggacc tgtgactctg cacctggttg 1380
ggcattttact ggcttttcta gacttgctt tcccccgagg gccattcat tcaatcttgc 1440
caatgacctt tgaggctgtc aagcaggacc atggcttcat gttgtaccga acctatatga 1500
ccataccat ttttgagcca acaccattct ggggtccaaa taatggagtc catgaccgtg 1560
cctatgtgat ggtggatggg gtgttccagg gtgttgtgga gcgaaatat agagacaaac 1620
tatttttgac ggggaaaactg ggggtccaaac tggatatctt ggtggagaac atggggaggc 1680
tcagcttttg gtctaacagc agtgacttca agggcctgtt gaagccacca attctggggc 1740
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aaattagccg ggcgtgatgg tgggcacctc taatccagc tacttgggag gctgagggca 2400
ggagaattgc ttgaatccag gaggcagagg ttgcagttag tggagggttg accactgcac 2460
tccagcctgg ctgacagtga gacactccat ctcaaaaaaa aaaaa 2505

```

&lt;210&gt; 177

&lt;211&gt; 654

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 177

```

Met Ala Pro Lys Lys Leu Ser Cys Leu Arg Ser Leu Leu Leu Pro Leu
  1              5              10              15

```

```

Ser Leu Thr Leu Leu Leu Pro Gln Ala Asp Thr Arg Ser Phe Val Val
      20              25              30

```

```

Asp Arg Gly His Asp Arg Phe Leu Leu Asp Gly Ala Pro Phe Arg Tyr
      35              40              45

```

```

Val Ser Gly Ser Leu His Tyr Phe Arg Val Pro Arg Val Leu Trp Ala
      50              55              60

```

Asp Arg Leu Leu Lys Met Arg Trp Ser Gly Leu Asn Ala Ile Gln Phe  
 65 70 75 80  
 Tyr Val Pro Trp Asn Tyr His Glu Pro Gln Pro Gly Val Tyr Asn Phe  
 85 90 95  
 Asn Gly Ser Arg Asp Leu Ile Ala Phe Leu Asn Glu Ala Ala Leu Ala  
 100 105 110  
 Asn Leu Leu Val Ile Leu Arg Pro Gly Pro Tyr Ile Cys Ala Glu Trp  
 115 120 125  
 Glu Met Gly Gly Leu Pro Ser Trp Leu Leu Arg Lys Pro Glu Ile His  
 130 135 140  
 Leu Arg Thr Ser Asp Pro Asp Phe Leu Ala Ala Val Asp Ser Trp Phe  
 145 150 155 160  
 Lys Val Leu Leu Pro Lys Ile Tyr Pro Trp Leu Tyr His Asn Gly Gly  
 165 170 175  
 Asn Ile Ile Ser Ile Gln Val Glu Asn Glu Tyr Gly Ser Tyr Arg Ala  
 180 185 190  
 Cys Asp Phe Ser Tyr Met Arg His Leu Ala Gly Leu Phe Arg Ala Leu  
 195 200 205  
 Leu Gly Glu Lys Ile Leu Leu Phe Thr Thr Asp Gly Pro Glu Gly Leu  
 210 215 220  
 Lys Cys Gly Ser Leu Arg Gly Leu Tyr Thr Thr Val Asp Phe Gly Pro  
 225 230 235 240  
 Ala Asp Asn Met Thr Lys Ile Phe Thr Leu Leu Arg Lys Tyr Glu Pro  
 245 250 255  
 His Gly Pro Leu Val Asn Ser Glu Tyr Tyr Thr Gly Trp Leu Asp Tyr  
 260 265 270  
 Trp Gly Gln Asn His Ser Thr Arg Ser Val Ser Ala Val Thr Lys Gly  
 275 280 285  
 Leu Glu Asn Met Leu Lys Leu Gly Ala Ser Val Asn Met Tyr Met Phe  
 290 295 300  
 His Gly Gly Thr Asn Phe Gly Tyr Trp Asn Gly Ala Asp Lys Lys Gly  
 305 310 315 320  
 Arg Phe Leu Pro Ile Thr Thr Ser Tyr Asp Tyr Asp Ala Pro Ile Ser  
 325 330 335  
 Glu Ala Gly Asp Pro Thr Pro Lys Leu Phe Ala Leu Arg Asp Val Ile

340	345	350
Ser Lys Phe Gln Glu Val Pro Leu Gly Pro Leu Pro Pro Pro Ser Pro		
355	360	365
Lys Met Met Leu Gly Pro Val Thr Leu His Leu Val Gly His Leu Leu		
370	375	380
Ala Phe Leu Asp Leu Leu Cys Pro Arg Gly Pro Ile His Ser Ile Leu		
385	390	395
Pro Met Thr Phe Glu Ala Val Lys Gln Asp His Gly Phe Met Leu Tyr		
405	410	415
Arg Thr Tyr Met Thr His Thr Ile Phe Glu Pro Thr Pro Phe Trp Val		
420	425	430
Pro Asn Asn Gly Val His Asp Arg Ala Tyr Val Met Val Asp Gly Val		
435	440	445
Phe Gln Gly Val Val Glu Arg Asn Met Arg Asp Lys Leu Phe Leu Thr		
450	455	460
Gly Lys Leu Gly Ser Lys Leu Asp Ile Leu Val Glu Asn Met Gly Arg		
465	470	475
Leu Ser Phe Gly Ser Asn Ser Ser Asp Phe Lys Gly Leu Leu Lys Pro		
485	490	495
Pro Ile Leu Gly Gln Thr Ile Leu Thr Gln Trp Met Met Phe Pro Leu		
500	505	510
Lys Ile Asp Asn Leu Val Lys Trp Trp Phe Pro Leu Gln Leu Pro Lys		
515	520	525
Trp Pro Tyr Pro Gln Ala Pro Ser Gly Pro Thr Phe Tyr Ser Lys Thr		
530	535	540
Phe Pro Ile Leu Gly Ser Val Gly Asp Thr Phe Leu Tyr Leu Pro Gly		
545	550	555
Trp Thr Lys Gly Gln Val Trp Ile Asn Gly Phe Asn Leu Gly Arg Tyr		
565	570	575
Trp Thr Lys Gln Gly Pro Gln Gln Thr Leu Tyr Val Pro Arg Phe Leu		
580	585	590
Leu Phe Pro Arg Gly Ala Leu Asn Lys Ile Thr Leu Leu Glu Leu Glu		
595	600	605
Asp Val Pro Leu Gln Pro Gln Val Gln Phe Leu Asp Lys Pro Ile Leu		
610	615	620

Asn Ser Thr Ser Thr Leu His Arg Thr His Ile Asn Ser Leu Ser Ala  
 625 630 635 640

Asp Thr Leu Ser Ala Ser Glu Pro Met Glu Leu Ser Gly His  
 645 650

<210> 178  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 178  
 tggctactcc aagaccctgg catg 24

<210> 179  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 179  
 tggacaaatc cccttgctca gcc 24

<210> 180  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 180  
 gggcttcacc gaagcagtgg acctttattt tgaccacctg atgtccaggg 50

<210> 181  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 181  
 ccagctatga ctatgatgca cc 22



<210> 182  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 182  
 tggcaccag aatggtgttg gctc

24

<210> 183  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 183  
 cgagatgtca tcagcaagtt ccaggaagtt cctttgggac ctttacctcc

50

<210> 184  
 <211> 1947  
 <212> DNA  
 <213> Homo sapiens

<400> 184  
 gctttgaaca cgtctgcaag cccaaagttg agcatctgat tggttatgag gtatttgagt 60  
 gcaccacaaa tatggcttac atgttgaaaa agcttctcat cagttacata tccattattt 120  
 gtgtttatgg ctttatctgc ctctacactc tcttctgggt attcaggata ctttgaagg 180  
 aatattcttt cgaaaaagtc agagaagaga gcagttttag tgacattcca gatgtcaaaa 240  
 acgattttgc gttccttctt cacatggtag accagtatga ccagctatat tccaagcgtt 300  
 ttggtgtgtt cttgtcagaa gttagtgaaa ataaacttag ggaaattagt ttgaaccatg 360  
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 tgcattctgt catgctgtcg ggggtgcccg atgctgtctt tgacctcaca gacctggatg 480  
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 cctgggtgta tttgctcaaa aaccttcgag agttgtactt aataggcaat ttgaactctg 720  
 aaaacaataa gatgatagga cttgaatctc tccgagagtt gcggcacctt aagattctcc 780  
 acgtgaagag caatttgacc aaagttccct ccaacattac agatgtggct ccacatctta 840  
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 tagatgtgag ctacaacaac atttcaatga ttccaataga aataggattg cttcagaacc 1260  
 tgcagcattt gcatatcact gggaacaaa tggacattct gccaaaacaa ttgtttaaat 1320

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gcataaagtt gaggactttg aatctgggac agaactgcat cacctcactc ccagagaaaag 1380
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cagcccagct gggccagtggt cggatgctca agaaaagcgg gcttggtgtg gaagatcacc 1500
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aatgtttgta ggggttttaag tcattcattt ccaaattcatt ttttttttct ttttggggaa 1800
aggggaaggaa aaattataat cactaatctt gggtcttttt aaattgtttg taacttggat 1860
gctgccgcta ctgaatgttt acaaattgct tgcttgctaa agtaaattgat taaattgaca 1920
ttttcttact aaaaaaaaaa aaaaaaaa 1947

```

&lt;210&gt; 185

&lt;211&gt; 501

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 185

```

Met Ala Tyr Met Leu Lys Lys Leu Leu Ile Ser Tyr Ile Ser Ile Ile
  1             5             10             15

```

```

Cys Val Tyr Gly Phe Ile Cys Leu Tyr Thr Leu Phe Trp Leu Phe Arg
          20             25             30

```

```

Ile Pro Leu Lys Glu Tyr Ser Phe Glu Lys Val Arg Glu Glu Ser Ser
          35             40             45

```

```

Phe Ser Asp Ile Pro Asp Val Lys Asn Asp Phe Ala Phe Leu Leu His
          50             55             60

```

```

Met Val Asp Gln Tyr Asp Gln Leu Tyr Ser Lys Arg Phe Gly Val Phe
          65             70             75             80

```

```

Leu Ser Glu Val Ser Glu Asn Lys Leu Arg Glu Ile Ser Leu Asn His
          85             90             95

```

```

Glu Trp Thr Phe Glu Lys Leu Arg Gln His Ile Ser Arg Asn Ala Gln
          100             105             110

```

```

Asp Lys Gln Glu Leu His Leu Phe Met Leu Ser Gly Val Pro Asp Ala
          115             120             125

```

```

Val Phe Asp Leu Thr Asp Leu Asp Val Leu Lys Leu Glu Leu Ile Pro
          130             135             140

```

```

Glu Ala Lys Ile Pro Ala Lys Ile Ser Gln Met Thr Asn Leu Gln Glu
          145             150             155             160

```

```

Leu His Leu Cys His Cys Pro Ala Lys Val Glu Gln Thr Ala Phe Ser
          165             170             175

```

```

Phe Leu Arg Asp His Leu Arg Cys Leu His Val Lys Phe Thr Asp Val
          180             185             190

```

Ala Glu Ile Pro Ala Trp Val Tyr Leu Leu Lys Asn Leu Arg Glu Leu  
 195 200 205  
 Tyr Leu Ile Gly Asn Leu Asn Ser Glu Asn Asn Lys Met Ile Gly Leu  
 210 215 220  
 Glu Ser Leu Arg Glu Leu Arg His Leu Lys Ile Leu His Val Lys Ser  
 225 230 235 240  
 Asn Leu Thr Lys Val Pro Ser Asn Ile Thr Asp Val Ala Pro His Leu  
 245 250 255  
 Thr Lys Leu Val Ile His Asn Asp Gly Thr Lys Leu Leu Val Leu Asn  
 260 265 270  
 Ser Leu Lys Lys Met Met Asn Val Ala Glu Leu Glu Leu Gln Asn Cys  
 275 280 285  
 Glu Leu Glu Arg Ile Pro His Ala Ile Phe Ser Leu Ser Asn Leu Gln  
 290 295 300  
 Glu Leu Asp Leu Lys Ser Asn Asn Ile Arg Thr Ile Glu Glu Ile Ile  
 305 310 315 320  
 Ser Phe Gln His Leu Lys Arg Leu Thr Cys Leu Lys Leu Trp His Asn  
 325 330 335  
 Lys Ile Val Thr Ile Pro Pro Ser Ile Thr His Val Lys Asn Leu Glu  
 340 345 350  
 Ser Leu Tyr Phe Ser Asn Asn Lys Leu Glu Ser Leu Pro Val Ala Val  
 355 360 365  
 Phe Ser Leu Gln Lys Leu Arg Cys Leu Asp Val Ser Tyr Asn Asn Ile  
 370 375 380  
 Ser Met Ile Pro Ile Glu Ile Gly Leu Leu Gln Asn Leu Gln His Leu  
 385 390 395 400  
 His Ile Thr Gly Asn Lys Val Asp Ile Leu Pro Lys Gln Leu Phe Lys  
 405 410 415  
 Cys Ile Lys Leu Arg Thr Leu Asn Leu Gly Gln Asn Cys Ile Thr Ser  
 420 425 430  
 Leu Pro Glu Lys Val Gly Gln Leu Ser Gln Leu Thr Gln Leu Glu Leu  
 435 440 445  
 Lys Gly Asn Cys Leu Asp Arg Leu Pro Ala Gln Leu Gly Gln Cys Arg  
 450 455 460  
 Met Leu Lys Lys Ser Gly Leu Val Val Glu Asp His Leu Phe Asp Thr

```
<400> 189
cccacgcgtc  cggccttctc  tctggacttt  gcatttccat  tccttttcat  tgacaaaactg  60
acttttttta  tttctttttt  tccatctctg  ggccagcttg  ggatcctagg  ccgccttggg  120
aagacatttg  tgttttacac  acataaggat  ctgtgttttg  ggtttcttct  tcttcccttg  180
```

```

acattggcat tgetttagtgg ttgtgtgggg agggagacca cgtgggctca gtgcttgcct 240
gcacttatct gcctaggtac atcgaagtct tttgacctcc atacagtgat tatgcctgtc 300
atcgtctggtg gtatcctggc ggcttgtctc ctgtgatag ttgtcgtgct ctgtctttac 360
ttcaaaatcac acaacgcgct aaaagctgca aaggaacctg aagctgtggc tgtaaaaaat 420
cacaacccag acaaggtgtg gtgggccaa aacagccagg ccaaaaccat tgccacggag 480
tcttgtcctg ccttgcagt ctgtgaagga tatagaatgt gtgccagttt tgattcctcg 540
ccaccttgcct gttgcgacat aaatgagggc ctctgagtta ggaaaggtct ccttctcaaa 600
gcagagccct gaagacttca atgatgtcaa tgaggccacc tgttttgtat gtgcaggcac 660
agaagaaagg cacagctccc catcagtttc atggaataa actcagtgcc tgcagggaac 720
cagctgctgg agatccctac agagagcttc cactgggggc aaccttcca ggaaggagt 780
ggggagagag aacctcact gtggggaatg ctgataaacc agtcacacag ctgctctatt 840
ctcacacaaa tctacctctt gcgtggctgg aactgacgtt tccctggagg tgtccagaaa 900
gctgatgtaa cacagagcct ataaaagctg tgggtcctta aggtgccca gcgccttgc 960
aaaatggagc ttgtaagaag gctcatgcca ttgacctct taattctctc ctgtttggcg 1020
gagctgacaa tggcggaggc tgaaggcaat gcaagctgca cagtcagtct agggggtgcc 1080
aatatggcag agaccacaa agccatgatc ctgcaactca atcccagtga gaactgcacc 1140
tggacaatag aaagaccaga aaacaaaagc atcagaatta tcttttcta tgtccagett 1200
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tccagtacat tgacgtttca aatagttact gactcagcaa gaattcaaag aactgtcttt 1380
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accttgggaag gatccttcac cagccccaat taccaaaagc cgcactctga gctggcttat 1500
tgtgtgtggc acatacaagt ggagaaagat tacaagataa aactaaactt caaagagatt 1560
ttcctagaaa tagacaaaac gtgcaaat tttttcttg ccatctatga tggccctcc 1620
accaactctg gctgattgg acaagtctgt ggccgtgtga ctcccacct cgaatcgtca 1680
tcaaactctc tgactgtcgt gttgtctaca gattatgcca attcttaccg gggattttct 1740
gcttcttaca cctcaattta tgcagaaaac atcaacacta catctttaac ttgctcttct 1800
gacaggatga gagtattat aagcaaatcc tacttagagg cttttaactc taatgggaat 1860
aacttgcaac taaaagacc aacttgca ccaaaattat caaatgttgt ggaattttct 1920
gtccctctta atggatgtgg tacaatcaga aaggtagaag atcagtcaat tacttacacc 1980
aatataatca cttttctgc atcctcaact tctgaagtga tcaccgtca gaaacaactc 2040
cagattattg tgaagtgtga aatgggacat aattctacag tggagataat atacataaca 2100
gaagatgatg taatacaaa tcaaaatgca ctgggcaaat ataacaccag catggctctt 2160
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gatacctgta gagcctctcc cactctgac tttgcatctc caacctacga cctaatacaag 2340
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aaataccaga agctgcagaa ctattaacta acaggtccaa cctaagtga gacatgtttc 2820
tccaggatgc caaaggaaat gctacctcgt ggctacacat attatgaata aatgaggaag 2880
ggcctgaaag tgacacacag gcctgcatgt aaaaaaa 2917

```

&lt;210&gt; 190

&lt;211&gt; 607

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 190

Met Glu Leu Val Arg Arg Leu Met Pro Leu Thr Leu Leu Ile Leu Ser  
 1 5 10 15  
 Cys Leu Ala Glu Leu Thr Met Ala Glu Ala Glu Gly Asn Ala Ser Cys  
 20 25 30  
 Thr Val Ser Leu Gly Gly Ala Asn Met Ala Glu Thr His Lys Ala Met  
 35 40 45  
 Ile Leu Gln Leu Asn Pro Ser Glu Asn Cys Thr Trp Thr Ile Glu Arg  
 50 55 60  
 Pro Glu Asn Lys Ser Ile Arg Ile Ile Phe Ser Tyr Val Gln Leu Asp  
 65 70 75 80  
 Pro Asp Gly Ser Cys Glu Ser Glu Asn Ile Lys Val Phe Asp Gly Thr  
 85 90 95  
 Ser Ser Asn Gly Pro Leu Leu Gly Gln Val Cys Ser Lys Asn Asp Tyr  
 100 105 110  
 Val Pro Val Phe Glu Ser Ser Ser Ser Thr Leu Thr Phe Gln Ile Val  
 115 120 125  
 Thr Asp Ser Ala Arg Ile Gln Arg Thr Val Phe Val Phe Tyr Tyr Phe  
 130 135 140  
 Phe Ser Pro Asn Ile Ser Ile Pro Asn Cys Gly Gly Tyr Leu Asp Thr  
 145 150 155 160  
 Leu Glu Gly Ser Phe Thr Ser Pro Asn Tyr Pro Lys Pro His Pro Glu  
 165 170 175  
 Leu Ala Tyr Cys Val Trp His Ile Gln Val Glu Lys Asp Tyr Lys Ile  
 180 185 190  
 Lys Leu Asn Phe Lys Glu Ile Phe Leu Glu Ile Asp Lys Gln Cys Lys  
 195 200 205  
 Phe Asp Phe Leu Ala Ile Tyr Asp Gly Pro Ser Thr Asn Ser Gly Leu  
 210 215 220  
 Ile Gly Gln Val Cys Gly Arg Val Thr Pro Thr Phe Glu Ser Ser Ser  
 225 230 235 240  
 Asn Ser Leu Thr Val Val Leu Ser Thr Asp Tyr Ala Asn Ser Tyr Arg  
 245 250 255  
 Gly Phe Ser Ala Ser Tyr Thr Ser Ile Tyr Ala Glu Asn Ile Asn Thr  
 260 265 270  
 Thr Ser Leu Thr Cys Ser Ser Asp Arg Met Arg Val Ile Ile Ser Lys  
 275 280 285

Ser Tyr Leu Glu Ala Phe Asn Ser Asn Gly Asn Asn Leu Gln Leu Lys  
 290 295 300

Asp Pro Thr Cys Arg Pro Lys Leu Ser Asn Val Val Glu Phe Ser Val  
 305 310 315 320

Pro Leu Asn Gly Cys Gly Thr Ile Arg Lys Val Glu Asp Gln Ser Ile  
 325 330 335

Thr Tyr Thr Asn Ile Ile Thr Phe Ser Ala Ser Ser Thr Ser Glu Val  
 340 345 350

Ile Thr Arg Gln Lys Gln Leu Gln Ile Ile Val Lys Cys Glu Met Gly  
 355 360 365

His Asn Ser Thr Val Glu Ile Ile Tyr Ile Thr Glu Asp Asp Val Ile  
 370 375 380

Gln Ser Gln Asn Ala Leu Gly Lys Tyr Asn Thr Ser Met Ala Leu Phe  
 385 390 395 400

Glu Ser Asn Ser Phe Glu Lys Thr Ile Leu Glu Ser Pro Tyr Tyr Val  
 405 410 415

Asp Leu Asn Gln Thr Leu Phe Val Gln Val Ser Leu His Thr Ser Asp  
 420 425 430

Pro Asn Leu Val Val Phe Leu Asp Thr Cys Arg Ala Ser Pro Thr Ser  
 435 440 445

Asp Phe Ala Ser Pro Thr Tyr Asp Leu Ile Lys Ser Gly Cys Ser Arg  
 450 455 460

Asp Glu Thr Cys Lys Val Tyr Pro Leu Phe Gly His Tyr Gly Arg Phe  
 465 470 475 480

Gln Phe Asn Ala Phe Lys Phe Leu Arg Ser Met Ser Ser Val Tyr Leu  
 485 490 495

Gln Cys Lys Val Leu Ile Cys Asp Ser Ser Asp His Gln Ser Arg Cys  
 500 505 510

Asn Gln Gly Cys Val Ser Arg Ser Lys Arg Asp Ile Ser Ser Tyr Lys  
 515 520 525

Trp Lys Thr Asp Ser Ile Ile Gly Pro Ile Arg Leu Lys Arg Asp Arg  
 530 535 540

Ser Ala Ser Gly Asn Ser Gly Phe Gln His Glu Thr His Ala Glu Glu  
 545 550 555 560

Thr Pro Asn Gln Pro Phe Asn Ser Val His Leu Phe Ser Phe Met Val

	565		570		575										
Leu	Ala	Leu	Asn	Val	Val	Thr	Val	Ala	Thr	Ile	Thr	Val	Arg	His	Phe
			580					585					590		
Val	Asn	Gln	Arg	Ala	Asp	Tyr	Lys	Tyr	Gln	Lys	Leu	Gln	Asn	Tyr	
		595					600					605			

&lt;210&gt; 191

&lt;211&gt; 21

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 191

tctctattcc aaactgtggc g

21

&lt;210&gt; 192

&lt;211&gt; 22

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 192

tttgatgacg attcgaaggt gg

22

&lt;210&gt; 193

&lt;211&gt; 47

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 193

ggaaggatcc ttcaccagcc ccaattaccc aaagccgcat cctgagc

47

&lt;210&gt; 194

&lt;211&gt; 2362

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 194

gacggaagaa cagcgctccc gaggcgcgag gagcctgcag agaggacagc cggcctgcgc 60  
cgggacatgc ggccccagga gctccccagg ctgcggttcc cggtgctgct gttgctgttg 120  
ctgctgctgc cgcgcgcgcc gtgccttgcg cacagcgcca cgcgcttcga cccacctgg 180



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gagtccttgg acgcccgcga gctgcccgcg tggtttgacc aggccaagtt cggcatcttc 240
atccactggg gagtgctttc cgtgcccagc ttcggtagcg agtggttctg gtggtattgg 300
caaaaggaaa agataccgaa gtatgtggaa tttatgaaag ataattaccc tccagtttc 360
aaatatgaag attttggacc actattttaca gcaaaatfff ttaatgccaa ccagtgggca 420
gatatcttcc aggcctctgg tgccaaatac attgtcttaa cttccaaaca tcatgaaggc 480
tttaccttgt gggggtcaga atattcgtgg aactggaatg ccatagatga ggggcccaag 540
agggacattg tcaaggaact tgaggtagcc attaggaaca gaactgacct gcgttttgga 600
ctgtactatt ccttttttga atggtttcat ccgctcttcc ttgaggatga atccagttca 660
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aactatcagc ctgaggttct gtggtcggat ggtgacggag gagcaccgga tcaatactgg 780
aacagcacag gcttcttggc ctggttatat aatgaaagcc cagttcgggg cacagtagtc 840
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gatcggtata acccaggaca tcttttgcca cataaatggg aaaactgcat gacaatagac 960
aaactgtcct ggggctatag gagggaagct ggaatctctg actatcttac aattgaagaa 1020
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atgtctaagg ctagggaacta tcaggtgtct ataattgtag cacatggaga aagcaatgta 1560
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caaacgtttt aattttttaa accttttttg ctcttttgta ataacactta gcttaaaaca 2340
taaactcatt gtgcaaatgt aa 2362

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&lt;210&gt; 195

&lt;211&gt; 467

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 195

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Met Arg Pro Gln Glu Leu Pro Arg Leu Ala Phe Pro Leu Leu Leu Leu
1           5           10          15

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```

Leu Leu Leu Leu Leu Pro Pro Pro Pro Cys Pro Ala His Ser Ala Thr
20           25           30

```

```

Arg Phe Asp Pro Thr Trp Glu Ser Leu Asp Ala Arg Gln Leu Pro Ala
35           40           45

```

Trp Phe Asp Gln Ala Lys Phe Gly Ile Phe Ile His Trp Gly Val Phe  
 50 55 60  
 Ser Val Pro Ser Phe Gly Ser Glu Trp Phe Trp Trp Tyr Trp Gln Lys  
 65 70 75 80  
 Glu Lys Ile Pro Lys Tyr Val Glu Phe Met Lys Asp Asn Tyr Pro Pro  
 85 90 95  
 Ser Phe Lys Tyr Glu Asp Phe Gly Pro Leu Phe Thr Ala Lys Phe Phe  
 100 105 110  
 Asn Ala Asn Gln Trp Ala Asp Ile Phe Gln Ala Ser Gly Ala Lys Tyr  
 115 120 125  
 Ile Val Leu Thr Ser Lys His His Glu Gly Phe Thr Leu Trp Gly Ser  
 130 135 140  
 Glu Tyr Ser Trp Asn Trp Asn Ala Ile Asp Glu Gly Pro Lys Arg Asp  
 145 150 155 160  
 Ile Val Lys Glu Leu Glu Val Ala Ile Arg Asn Arg Thr Asp Leu Arg  
 165 170 175  
 Phe Gly Leu Tyr Tyr Ser Leu Phe Glu Trp Phe His Pro Leu Phe Leu  
 180 185 190  
 Glu Asp Glu Ser Ser Ser Phe His Lys Arg Gln Phe Pro Val Ser Lys  
 195 200 205  
 Thr Leu Pro Glu Leu Tyr Glu Leu Val Asn Asn Tyr Gln Pro Glu Val  
 210 215 220  
 Leu Trp Ser Asp Gly Asp Gly Gly Ala Pro Asp Gln Tyr Trp Asn Ser  
 225 230 235 240  
 Thr Gly Phe Leu Ala Trp Leu Tyr Asn Glu Ser Pro Val Arg Gly Thr  
 245 250 255  
 Val Val Thr Asn Asp Arg Trp Gly Ala Gly Ser Ile Cys Lys His Gly  
 260 265 270  
 Gly Phe Tyr Thr Cys Ser Asp Arg Tyr Asn Pro Gly His Leu Leu Pro  
 275 280 285  
 His Lys Trp Glu Asn Cys Met Thr Ile Asp Lys Leu Ser Trp Gly Tyr  
 290 295 300  
 Arg Arg Glu Ala Gly Ile Ser Asp Tyr Leu Thr Ile Glu Glu Leu Val  
 305 310 315 320  
 Lys Gln Leu Val Glu Thr Val Ser Cys Gly Gly Asn Leu Leu Met Asn  
 325 330 335

Ile Gly Pro Thr Leu Asp Gly Thr Ile Ser Val Val Phe Glu Glu Arg  
 340 345 350

Leu Arg Gln Val Gly Ser Trp Leu Lys Val Asn Gly Glu Ala Ile Tyr  
 355 360 365

Glu Thr Tyr Thr Trp Arg Ser Gln Asn Asp Thr Val Thr Pro Asp Val  
 370 375 380

Trp Tyr Thr Ser Lys Pro Lys Glu Lys Leu Val Tyr Ala Ile Phe Leu  
 385 390 395 400

Lys Trp Pro Thr Ser Gly Gln Leu Phe Leu Gly His Pro Lys Ala Ile  
 405 410 415

Leu Gly Ala Thr Glu Val Lys Leu Leu Gly His Gly Gln Pro Leu Asn  
 420 425 430

Trp Ile Ser Leu Glu Gln Asn Gly Ile Met Val Glu Leu Pro Gln Leu  
 435 440 445

Thr Ile His Gln Met Pro Cys Lys Trp Gly Trp Ala Leu Ala Leu Thr  
 450 455 460

Asn Val Ile  
 465

<210> 196

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 196

tggtttgacc aggccaagtt cgg

23

<210> 197

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 197

ggattcatcc tcaaggaaga gcgg

24

<210> 198

<211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 198  
 aacttgacgc atcagccact ctgc

24

<210> 199  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 199  
 ttccgtgccc agcttcggta gcgagtgggt ctggtggtat tggca

45

<210> 200  
 <211> 2372  
 <212> DNA  
 <213> Homo sapiens

<400> 200  
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<210> 201

<211> 322

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic protein

<400> 201

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Thr Arg Leu Leu Val Gln Gly Ser Leu Arg Ala Glu Glu Leu Ser Ile
          20              25              30

Gln Val Ser Cys Arg Ile Met Gly Ile Thr Leu Val Ser Lys Lys Ala
          35              40              45

Asn Gln Gln Leu Asn Phe Thr Glu Ala Lys Glu Ala Cys Arg Leu Leu
          50              55              60

Gly Leu Ser Leu Ala Gly Lys Asp Gln Val Glu Thr Ala Leu Lys Ala
          65              70              75              80

Ser Phe Glu Thr Cys Ser Tyr Gly Trp Val Gly Asp Gly Phe Val Val
          85              90              95

Ile Ser Arg Ile Ser Pro Asn Pro Lys Cys Gly Lys Asn Gly Val Gly
          100             105             110

Val Leu Ile Trp Lys Val Pro Val Ser Arg Gln Phe Ala Ala Tyr Cys
          115              120              125

Tyr Asn Ser Ser Asp Thr Trp Thr Asn Ser Cys Ile Pro Glu Ile Ile
          130             135             140

```

Thr Thr Lys Asp Pro Ile Phe Asn Thr Gln Thr Ala Thr Gln Thr Thr  
 145 150 155 160  
 Glu Phe Ile Val Ser Asp Ser Thr Tyr Ser Val Ala Ser Pro Tyr Ser  
 165 170 175  
 Thr Ile Pro Ala Pro Thr Thr Thr Pro Pro Ala Pro Ala Ser Thr Ser  
 180 185 190  
 Ile Pro Arg Arg Lys Lys Leu Ile Cys Val Thr Glu Val Phe Met Glu  
 195 200 205  
 Thr Ser Thr Met Ser Thr Glu Thr Glu Pro Phe Val Glu Asn Lys Ala  
 210 215 220  
 Ala Phe Lys Asn Glu Ala Ala Gly Phe Gly Gly Val Pro Thr Ala Leu  
 225 230 235 240  
 Leu Val Leu Ala Leu Leu Phe Phe Gly Ala Ala Ala Gly Leu Gly Phe  
 245 250 255  
 Cys Tyr Val Lys Arg Tyr Val Lys Ala Phe Pro Phe Thr Asn Lys Asn  
 260 265 270  
 Gln Gln Lys Glu Met Ile Glu Thr Lys Val Val Lys Glu Glu Lys Ala  
 275 280 285  
 Asn Asp Ser Asn Pro Asn Glu Glu Ser Lys Lys Thr Asp Lys Asn Pro  
 290 295 300  
 Glu Glu Ser Lys Ser Pro Ser Lys Thr Thr Val Arg Cys Leu Glu Ala  
 305 310 315 320  
 Glu Val

&lt;210&gt; 202

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

&lt;400&gt; 202

gagctttcca tccaggtgtc atgc

24

&lt;210&gt; 203

&lt;211&gt; 22

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 203

gtcagtgaca gtacctactc gg

22

<210> 204

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 204

tggagcagga ggagtagtag tagg

24

<210> 205

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 205

aggaggcctg taggctgctg ggactaagtt tggccggcaa ggaccaagtt

50

<210> 206

<211> 1620

<212> DNA

<213> Homo sapiens

<220>

<221> modified\_base

<222> (973)

<223> a, t, c or g

<220>

<221> modified\_base

<222> (977)

<223> a, t, c or g

<220>

<221> modified\_base

<222> (996)

<223> a, t, c or g

<220>

<221> modified\_base

&lt;222&gt; (1003)

&lt;223&gt; a, t, c or g

&lt;400&gt; 206

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ggaaactgcc gccgctctgc cacggtctgc ccaccaacg cgaagacggg aaccctgtgtg 180
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actttccttt gtgtggtagg acttggagga gaaatccct ggactttcac taaccctctg 1560
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```

&lt;210&gt; 207

&lt;211&gt; 296

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 207

```

Met Ala Val Leu Ala Pro Leu Ile Ala Leu Val Tyr Ser Val Pro Arg
 1              5              10              15

Leu Ser Arg Trp Leu Ala Gln Pro Tyr Tyr Leu Leu Ser Ala Leu Leu
 20              25              30

Ser Ala Ala Phe Leu Leu Val Arg Lys Leu Pro Pro Leu Cys His Gly
 35              40              45

Leu Pro Thr Gln Arg Glu Asp Gly Asn Pro Cys Asp Phe Asp Trp Arg
 50              55              60

Glu Val Glu Ile Leu Met Phe Leu Ser Ala Ile Val Met Met Lys Asn
 65              70              75              80

```



Arg Arg Ser Ile Thr Val Glu Gln His Ile Gly Asn Ile Phe Met Phe  
                             85                            90                            95  
 Ser Lys Val Ala Asn Thr Ile Leu Phe Phe Arg Leu Asp Ile Arg Met  
                             100                            105                            110  
 Gly Leu Leu Tyr Ile Thr Leu Cys Ile Val Phe Leu Met Thr Cys Lys  
                             115                            120                            125  
 Pro Pro Leu Tyr Met Gly Pro Glu Tyr Ile Lys Tyr Phe Asn Asp Lys  
                             130                            135                            140  
 Thr Ile Asp Glu Glu Leu Glu Arg Asp Lys Arg Val Thr Trp Ile Val  
                             145                            150                            155                            160  
 Glu Phe Phe Ala Asn Trp Ser Asn Asp Cys Gln Ser Phe Ala Pro Ile  
                             165                            170                            175  
 Tyr Ala Asp Leu Ser Leu Lys Tyr Asn Cys Thr Gly Leu Asn Phe Gly  
                             180                            185                            190  
 Lys Val Asp Val Gly Arg Tyr Thr Asp Val Ser Thr Arg Tyr Lys Val  
                             195                            200                            205  
 Ser Thr Ser Pro Leu Thr Lys Gln Leu Pro Thr Leu Ile Leu Phe Gln  
                             210                            215                            220  
 Gly Gly Lys Glu Ala Met Arg Arg Pro Gln Ile Asp Lys Lys Gly Arg  
                             225                            230                            235                            240  
 Ala Val Ser Trp Thr Phe Ser Glu Glu Asn Val Ile Arg Glu Phe Asn  
                             245                            250                            255  
 Leu Asn Glu Leu Tyr Gln Arg Ala Lys Lys Leu Ser Lys Ala Gly Asp  
                             260                            265                            270  
 Asn Ile Pro Glu Glu Gln Pro Val Ala Ser Thr Pro Thr Thr Val Ser  
                             275                            280                            285  
 Asp Gly Glu Asn Lys Lys Asp Lys  
                             290                            295

&lt;210&gt; 208

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

&lt;400&gt; 208

gcttgatat tcgcatgggc ctac

<210> 209  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 209  
 tggagacaat atccctgagg 20

<210> 210  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 210  
 aacagttggc cacagcatgg cagg 24

<210> 211  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 211  
 ccattgatga ggaactagaa cgggacaaga gggtcacttg gattgtggag 50

<210> 212  
 <211> 1985  
 <212> DNA  
 <213> Homo sapiens

<400> 212  
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 cccattgctc ctgctgcccc gctcctacgg actgcccttc tacaacggct tctactactc 180  
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aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1980
aaaaaa

```

&lt;210&gt; 213

&lt;211&gt; 360

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 213

```

Met Gly Leu Leu Leu Leu Val Pro Leu Leu Leu Leu Pro Gly Ser Tyr
  1                      5                      10                      15

```

```

Gly Leu Pro Phe Tyr Asn Gly Phe Tyr Tyr Ser Asn Ser Ala Asn Asp
          20                      25                      30

```

```

Gln Asn Leu Gly Asn Gly His Gly Lys Asp Leu Leu Asn Gly Val Lys
          35                      40                      45

```

```

Leu Val Val Glu Thr Pro Glu Glu Thr Leu Phe Thr Tyr Gln Gly Ala
          50                      55                      60

```

```

Ser Val Ile Leu Pro Cys Arg Tyr Arg Tyr Glu Pro Ala Leu Val Ser
          65                      70                      75                      80

```

```

Pro Arg Arg Val Arg Val Lys Trp Trp Lys Leu Ser Glu Asn Gly Ala
          85                      90                      95

```

```

Pro Glu Lys Asp Val Leu Val Ala Ile Gly Leu Arg His Arg Ser Phe
          100                      105                      110

```

```

Gly Asp Tyr Gln Gly Arg Val His Leu Arg Gln Asp Lys Glu His Asp

```

115	120	125
Val Ser Leu Glu Ile Gln Asp Leu Arg Leu Glu Asp Tyr Gly Arg Tyr		
130	135	140
Arg Cys Glu Val Ile Asp Gly Leu Glu Asp Glu Ser Gly Leu Val Glu		
145	150	155
Leu Glu Leu Arg Gly Val Val Phe Pro Tyr Gln Ser Pro Asn Gly Arg		
	165	170
Tyr Gln Phe Asn Phe His Glu Gly Gln Gln Val Cys Ala Glu Gln Ala		
	180	185
Ala Val Val Ala Ser Phe Glu Gln Leu Phe Arg Ala Trp Glu Glu Gly		
	195	200
Leu Asp Trp Cys Asn Ala Gly Trp Leu Gln Asp Ala Thr Val Gln Tyr		
	210	215
Pro Ile Met Leu Pro Arg Gln Pro Cys Gly Gly Pro Gly Leu Ala Pro		
	225	230
Gly Val Arg Ser Tyr Gly Pro Arg His Arg Arg Leu His Arg Tyr Asp		
	245	250
Val Phe Cys Phe Ala Thr Ala Leu Lys Gly Arg Val Tyr Tyr Leu Glu		
	260	265
His Pro Glu Lys Leu Thr Leu Thr Glu Ala Arg Glu Ala Cys Gln Glu		
	275	280
Asp Asp Ala Thr Ile Ala Lys Val Gly Gln Leu Phe Ala Ala Trp Lys		
	290	295
Phe His Gly Leu Asp Arg Cys Asp Ala Gly Trp Leu Ala Asp Gly Ser		
	305	310
Val Arg Tyr Pro Val Val His Pro His Pro Asn Cys Gly Pro Pro Glu		
	325	330
Pro Gly Val Arg Ser Phe Gly Phe Pro Asp Pro Gln Ser Arg Leu Tyr		
	340	345
Gly Val Tyr Cys Tyr Arg Gln His		
	355	360

&lt;210&gt; 214

&lt;211&gt; 18

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 214  
tgcttegcta ctgccctc 18

<210> 215  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 215  
ttcccttggtg ggttggag 18

<210> 216  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 216  
agggctggaa gccagttc 18

<210> 217  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 217  
agccagtgag gaaatgag 18

<210> 218  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 218  
tgtccaaagt acacacacct gagg 24

<210> 219  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 219  
 gatgccacga tcgccaaggt gggacagctc tttgccgcct ggaag 45

<210> 220  
 <211> 1503  
 <212> DNA  
 <213> Homo sapiens

<400> 220  
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 tggccagggg aggggtgcacc aggcggcccc cctgagcgac gctccccatg atgacgcca 180  
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 gtactcagcc gagcctgggg aggaggagcc ggcgtgggtg cagacggaga ggcagcagtt 780  
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 aaa 1503

<210> 221  
 <211> 328  
 <212> PRT  
 <213> Homo sapiens

<400> 221  
 Met Met Trp Arg Pro Ser Val Leu Leu Leu Leu Leu Leu Arg His

1	5	10	15
Gly Ala Gln Gly Lys Pro Ser Pro Asp Ala Gly Pro His Gly Gln Gly	20	25	30
Arg Val His Gln Ala Ala Pro Leu Ser Asp Ala Pro His Asp Asp Ala	35	40	45
His Gly Asn Phe Gln Tyr Asp His Glu Ala Phe Leu Gly Arg Glu Val	50	55	60
Ala Lys Glu Phe Asp Gln Leu Thr Pro Glu Glu Ser Gln Ala Arg Leu	65	70	75
Gly Arg Ile Val Asp Arg Met Asp Arg Ala Gly Asp Gly Asp Gly Trp	85	90	95
Val Ser Leu Ala Glu Leu Arg Ala Trp Ile Ala His Thr Gln Gln Arg	100	105	110
His Ile Arg Asp Ser Val Ser Ala Ala Trp Asp Thr Tyr Asp Thr Asp	115	120	125
Arg Asp Gly Arg Val Gly Trp Glu Glu Leu Arg Asn Ala Thr Tyr Gly	130	135	140
His Tyr Ala Pro Gly Glu Glu Phe His Asp Val Glu Asp Ala Glu Thr	145	150	155
Tyr Lys Lys Met Leu Ala Arg Asp Glu Arg Arg Phe Arg Val Ala Asp	165	170	175
Gln Asp Gly Asp Ser Met Ala Thr Arg Glu Glu Leu Thr Ala Phe Leu	180	185	190
His Pro Glu Glu Phe Pro His Met Arg Asp Ile Val Ile Ala Glu Thr	195	200	205
Leu Glu Asp Leu Asp Arg Asn Lys Asp Gly Tyr Val Gln Val Glu Glu	210	215	220
Tyr Ile Ala Asp Leu Tyr Ser Ala Glu Pro Gly Glu Glu Glu Pro Ala	225	230	235
Trp Val Gln Thr Glu Arg Gln Gln Phe Arg Asp Phe Arg Asp Leu Asn	245	250	255
Lys Asp Gly His Leu Asp Gly Ser Glu Val Gly His Trp Val Leu Pro	260	265	270
Pro Ala Gln Asp Gln Pro Leu Val Glu Ala Asn His Leu Leu His Glu	275	280	285

Ser Asp Thr Asp Lys Asp Gly Arg Leu Ser Lys Ala Glu Ile Leu Gly  
 290 295 300

Asn Trp Asn Met Phe Val Gly Ser Gln Ala Thr Asn Tyr Gly Glu Asp  
 305 310 315 320

Leu Thr Arg His His Asp Glu Leu  
 325

<210> 222

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 222

cgcaggccct catggccagg

20

<210> 223

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 223

gaaatcctgg gtaattgg

18

<210> 224

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 224

gtgcgcggtg ctcacagctc atc

23

<210> 225

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe



<400> 225  
 cccccctgag cgacgctccc ccatgatgac gccacggga actt

44

<210> 226  
 <211> 2403  
 <212> DNA  
 <213> Homo sapiens

<400> 226  
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 gggcggcggg cgcgggtgag agggatccct gacgcctctg tccctgttcc tttgtcgctc 120  
 ccagcctgtc tgtcgctcgt ttggcgcccc cgcctccccg cggtgccggg ttgcacaccg 180  
 atcctgggct tcgctcgatt tgcgcgcgag gcgcctccca gacctagagg ggcgctggcc 240  
 tggagcagcg ggtcgtctgt gtccctctct ctctgcgcgc cgcgcgggga tccgaagggt 300  
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 tccagtctca aatgctttct agatggctct cttctttcac agtaactaaa ggcaaaagta 780  
 gtacacagga ggccacagga caagcagtg tccacagcaca tccaccaaca ggtaaacgac 840  
 taaagaaaac acccgagaag aaaactggca ataaagattg taaagcagac attgcatttc 900  
 tgattgatgg aagctttaat attgggcagc gccgatttaa tttacagaag aattttgttg 960  
 gaaaagtggc tctaattgtg ggaattggaa cagaaggacc acatgtgggc cttgttcaag 1020  
 ccagtgaaca tcccaaaata gaattttact tgaaaaactt tacatcagcc aaagatgttt 1080  
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 tccatagta tgtcacagat gggcagtcct atgatgatgt ccaaggccct gcagctgctg 1860  
 cacatgatgc aggaatcact atcttctctg ttgggtgtggc ttgggcacct ctggatgacc 1920  
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 aaa 2403

<210> 227

<211> 550  
 <212> PRT  
 <213> Homo sapiens

<400> 227

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Leu Leu Pro Gly Pro Ala Gly Ser Glu Gly Ala Ala Pro Ile Ala Ile  
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Thr Cys Phe Thr Arg Gly Leu Asp Ile Arg Lys Glu Lys Ala Asp Val  
 35 40 45

Leu Cys Pro Gly Gly Cys Pro Leu Glu Glu Phe Ser Val Tyr Gly Asn  
 50 55 60

Ile Val Tyr Ala Ser Val Ser Ser Ile Cys Gly Ala Ala Val His Arg  
 65 70 75 80

Gly Val Ile Ser Asn Ser Gly Gly Pro Val Arg Val Tyr Ser Leu Pro  
 85 90 95

Gly Arg Glu Asn Tyr Ser Ser Val Asp Ala Asn Gly Ile Gln Ser Gln  
 100 105 110

Met Leu Ser Arg Trp Ser Ala Ser Phe Thr Val Thr Lys Gly Lys Ser  
 115 120 125

Ser Thr Gln Glu Ala Thr Gly Gln Ala Val Ser Thr Ala His Pro Pro  
 130 135 140

Thr Gly Lys Arg Leu Lys Lys Thr Pro Glu Lys Lys Thr Gly Asn Lys  
 145 150 155 160

Asp Cys Lys Ala Asp Ile Ala Phe Leu Ile Asp Gly Ser Phe Asn Ile  
 165 170 175

Gly Gln Arg Arg Phe Asn Leu Gln Lys Asn Phe Val Gly Lys Val Ala  
 180 185 190

Leu Met Leu Gly Ile Gly Thr Glu Gly Pro His Val Gly Leu Val Gln  
 195 200 205

Ala Ser Glu His Pro Lys Ile Glu Phe Tyr Leu Lys Asn Phe Thr Ser  
 210 215 220

Ala Lys Asp Val Leu Phe Ala Ile Lys Glu Val Gly Phe Arg Gly Gly  
 225 230 235 240

Asn Ser Asn Thr Gly Lys Ala Leu Lys His Thr Ala Gln Lys Phe Phe  
 245 250 255

Thr Val Asp Ala Gly Val Arg Lys Gly Ile Pro Lys Val Val Val Val  
 260 265 270  
 Phe Ile Asp Gly Trp Pro Ser Asp Asp Ile Glu Glu Ala Gly Ile Val  
 275 280 285  
 Ala Arg Glu Phe Gly Val Asn Val Phe Ile Val Ser Val Ala Lys Pro  
 290 295 300  
 Ile Pro Glu Glu Leu Gly Met Val Gln Asp Val Thr Phe Val Asp Lys  
 305 310 315 320  
 Ala Val Cys Arg Asn Asn Gly Phe Phe Ser Tyr His Met Pro Asn Trp  
 325 330 335  
 Phe Gly Thr Thr Lys Tyr Val Lys Pro Leu Val Gln Lys Leu Cys Thr  
 340 345 350  
 His Glu Gln Met Met Cys Ser Lys Thr Cys Tyr Asn Ser Val Asn Ile  
 355 360 365  
 Ala Phe Leu Ile Asp Gly Ser Ser Ser Val Gly Asp Ser Asn Phe Arg  
 370 375 380  
 Leu Met Leu Glu Phe Val Ser Asn Ile Ala Lys Thr Phe Glu Ile Ser  
 385 390 395 400  
 Asp Ile Gly Ala Lys Ile Ala Ala Val Gln Phe Thr Tyr Asp Gln Arg  
 405 410 415  
 Thr Glu Phe Ser Phe Thr Asp Tyr Ser Thr Lys Glu Asn Val Leu Ala  
 420 425 430  
 Val Ile Arg Asn Ile Arg Tyr Met Ser Gly Gly Thr Ala Thr Gly Asp  
 435 440 445  
 Ala Ile Ser Phe Thr Val Arg Asn Val Phe Gly Pro Ile Arg Glu Ser  
 450 455 460  
 Pro Asn Lys Asn Phe Leu Val Ile Val Thr Asp Gly Gln Ser Tyr Asp  
 465 470 475 480  
 Asp Val Gln Gly Pro Ala Ala Ala Ala His Asp Ala Gly Ile Thr Ile  
 485 490 495  
 Phe Ser Val Gly Val Ala Trp Ala Pro Leu Asp Asp Leu Lys Asp Met  
 500 505 510  
 Ala Ser Lys Pro Lys Glu Ser His Ala Phe Phe Thr Arg Glu Phe Thr  
 515 520 525  
 Gly Leu Glu Pro Ile Val Ser Asp Val Ile Arg Gly Ile Cys Arg Asp  
 530 535 540

Phe Leu Glu Ser Gln Gln  
545 550

<210> 228  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 228 18  
tggtctcgca caccgatc

<210> 229  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 229 18  
ctgctgtcca caggggag

<210> 230  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 230 18  
ccttgaagca tactgctc

<210> 231  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 231 18  
gagatagcaa tttccgcc

<210> 232

<211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 232  
 ttctcaaga gggcagcc 18

<210> 233  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 233  
 cttggcacca atgtccgaga ttcc 24

<210> 234  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 234  
 gctctgagga aggtgacgcg cggggcctcc gaacccttgg ccttg 45

<210> 235  
 <211> 2586  
 <212> DNA  
 <213> Homo sapiens

<400> 235  
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 ctccagtcga gcccgggccg gctctcagct accgcgagga ggaggccacc ctcaatgaga 300  
 tggtccgcga ggttgaggaa ctgatggagg acacgcagca caaattgcgc agcgcggtgg 360  
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 tacctcccag ctatcacaat gagaccaaca cagacacgaa ggttggaat aataccatcc 480  
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 acgaggactg tgggcccagc atgtactgcc agtttgccag cttccagtac acctgccagc 660  
 catgccgggg ccagaggatg ctctgcaccc gggacagtga gtgctgtgga gaccagctgt 720

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aaaaaa

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&lt;210&gt; 236

&lt;211&gt; 350

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 236

```

Met Gln Arg Leu Gly Ala Thr Leu Leu Cys Leu Leu Leu Ala Ala Ala
  1             5             10             15

```

```

Val Pro Thr Ala Pro Ala Pro Ala Pro Thr Ala Thr Ser Ala Pro Val
          20             25             30

```

```

Lys Pro Gly Pro Ala Leu Ser Tyr Pro Gln Glu Glu Ala Thr Leu Asn
    35             40             45

```

```

Glu Met Phe Arg Glu Val Glu Glu Leu Met Glu Asp Thr Gln His Lys
    50             55             60

```

```

Leu Arg Ser Ala Val Glu Glu Met Glu Ala Glu Glu Ala Ala Ala Lys
    65             70             75             80

```

Ala Ser Ser Glu Val Asn Leu Ala Asn Leu Pro Pro Ser Tyr His Asn  
 85 90 95  
 Glu Thr Asn Thr Asp Thr Lys Val Gly Asn Asn Thr Ile His Val His  
 100 105 110  
 Arg Glu Ile His Lys Ile Thr Asn Asn Gln Thr Gly Gln Met Val Phe  
 115 120 125  
 Ser Glu Thr Val Ile Thr Ser Val Gly Asp Glu Glu Gly Arg Arg Ser  
 130 135 140  
 His Glu Cys Ile Ile Asp Glu Asp Cys Gly Pro Ser Met Tyr Cys Gln  
 145 150 155 160  
 Phe Ala Ser Phe Gln Tyr Thr Cys Gln Pro Cys Arg Gly Gln Arg Met  
 165 170 175  
 Leu Cys Thr Arg Asp Ser Glu Cys Cys Gly Asp Gln Leu Cys Val Trp  
 180 185 190  
 Gly His Cys Thr Lys Met Ala Thr Arg Gly Ser Asn Gly Thr Ile Cys  
 195 200 205  
 Asp Asn Gln Arg Asp Cys Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg  
 210 215 220  
 Gly Leu Leu Phe Pro Val Cys Thr Pro Leu Pro Val Glu Gly Glu Leu  
 225 230 235 240  
 Cys His Asp Pro Ala Ser Arg Leu Leu Asp Leu Ile Thr Trp Glu Leu  
 245 250 255  
 Glu Pro Asp Gly Ala Leu Asp Arg Cys Pro Cys Ala Ser Gly Leu Leu  
 260 265 270  
 Cys Gln Pro His Ser His Ser Leu Val Tyr Val Cys Lys Pro Thr Phe  
 275 280 285  
 Val Gly Ser Arg Asp Gln Asp Gly Glu Ile Leu Leu Pro Arg Glu Val  
 290 295 300  
 Pro Asp Glu Tyr Glu Val Gly Ser Phe Met Glu Glu Val Arg Gln Glu  
 305 310 315 320  
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 Pro Ala Ala Ala Ala Ala Leu Leu Gly Gly Glu Glu Ile  
 340 345 350

&lt;210&gt; 237

<211> 17  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 237  
ggagctgcac cccttgc

17

<210> 238  
<211> 49  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 238  
ggaggactgt gccaccatga gagactcttc aaaccaagg caaaattgg

49

<210> 239  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 239  
gcagagcggg gatgcagcgg cttg

24

<210> 240  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 240  
ttggcagctt catggagg

18

<210> 241  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 241  
cctgggcaaa aatgcaac

18



<210> 242  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 242  
 ctccagctcc tggcgcacct cctc

24

<210> 243  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 243  
 ggctctcagc taccgcgcag gagcgaggcc accctcaatg agatg

45

<210> 244  
 <211> 3679  
 <212> DNA  
 <213> Homo Sapien

<400> 244  
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 tctctctggg ctcagaagga ctctgaagat aacaataatt tcagcccatc 100  
 cactctcctt ccttcccaaa cacacatgtg catgtacaca cacacatata 150  
 cacacatata ccttctcttc cttcactgaa gactcacagt cactcactct 200  
 gtgagcaggt catagaaaag gacactaaag ccttaaggac aggcttggcc 250  
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 gaatccagga ggcggaggat gcagtcagct gagtgcaccg ctgcactcca 550  
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<210> 245

<211> 713

<212> PRT

<213> Homo Sapien

<400> 245

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Ala	Thr	Ala	Thr	Val	Pro	Val	Val	Pro	Trp	His	Val	Pro	Cys	Pro	20	25	30	
Pro	Gln	Cys	Ala	Cys	Gln	Ile	Arg	Pro	Trp	Tyr	Thr	Pro	Arg	Ser	35	40	45	
Ser	Tyr	Arg	Glu	Ala	Thr	Thr	Val	Asp	Cys	Asn	Asp	Leu	Phe	Leu	50	55	60	
Thr	Ala	Val	Pro	Pro	Ala	Leu	Pro	Ala	Gly	Thr	Gln	Thr	Leu	Leu	65	70	75	
Leu	Gln	Ser	Asn	Ser	Ile	Val	Arg	Val	Asp	Gln	Ser	Glu	Leu	Gly	80	85	90	
Tyr	Leu	Ala	Asn	Leu	Thr	Glu	Leu	Asp	Leu	Ser	Gln	Asn	Ser	Phe	95	100	105	
Ser	Asp	Ala	Arg	Asp	Cys	Asp	Phe	His	Ala	Leu	Pro	Gln	Leu	Leu	110	115	120	
Ser	Leu	His	Leu	Glu	Glu	Asn	Gln	Leu	Thr	Arg	Leu	Glu	Asp	His	125	130	135	
Ser	Phe	Ala	Gly	Leu	Ala	Ser	Leu	Gln	Glu	Leu	Tyr	Leu	Asn	His	140	145	150	

Asn Gln Leu Tyr Arg Ile Ala Pro Arg Ala Phe Ser Gly Leu Ser	155	160	165
Asn Leu Leu Arg Leu His Leu Asn Ser Asn Leu Leu Arg Ala Ile	170	175	180
Asp Ser Arg Trp Phe Glu Met Leu Pro Asn Leu Glu Ile Leu Met	185	190	195
Ile Gly Gly Asn Lys Val Asp Ala Ile Leu Asp Met Asn Phe Arg	200	205	210
Pro Leu Ala Asn Leu Arg Ser Leu Val Leu Ala Gly Met Asn Leu	215	220	225
Arg Glu Ile Ser Asp Tyr Ala Leu Glu Gly Leu Gln Ser Leu Glu	230	235	240
Ser Leu Ser Phe Tyr Asp Asn Gln Leu Ala Arg Val Pro Arg Arg	245	250	255
Ala Leu Glu Gln Val Pro Gly Leu Lys Phe Leu Asp Leu Asn Lys	260	265	270
Asn Pro Leu Gln Arg Val Gly Pro Gly Asp Phe Ala Asn Met Leu	275	280	285
His Leu Lys Glu Leu Gly Leu Asn Asn Met Glu Glu Leu Val Ser	290	295	300
Ile Asp Lys Phe Ala Leu Val Asn Leu Pro Glu Leu Thr Lys Leu	305	310	315
Asp Ile Thr Asn Asn Pro Arg Leu Ser Phe Ile His Pro Arg Ala	320	325	330
Phe His His Leu Pro Gln Met Glu Thr Leu Met Leu Asn Asn Asn	335	340	345
Ala Leu Ser Ala Leu His Gln Gln Thr Val Glu Ser Leu Pro Asn	350	355	360
Leu Gln Glu Val Gly Leu His Gly Asn Pro Ile Arg Cys Asp Cys	365	370	375
Val Ile Arg Trp Ala Asn Ala Thr Gly Thr Arg Val Arg Phe Ile	380	385	390
Glu Pro Gln Ser Thr Leu Cys Ala Glu Pro Pro Asp Leu Gln Arg	395	400	405
Leu Pro Val Arg Glu Val Pro Phe Arg Glu Met Thr Asp His Cys			

410	415	420
Leu Pro Leu Ile Ser Pro Arg Ser Phe	Pro Pro Ser Leu Gln Val	
425	430	435
Ala Ser Gly Glu Ser Met Val Leu His	Cys Arg Ala Leu Ala Glu	
440	445	450
Pro Glu Pro Glu Ile Tyr Trp Val Thr	Pro Ala Gly Leu Arg Leu	
455	460	465
Thr Pro Ala His Ala Gly Arg Arg Tyr	Arg Val Tyr Pro Glu Gly	
470	475	480
Thr Leu Glu Leu Arg Arg Val Thr Ala	Glu Glu Ala Gly Leu Tyr	
485	490	495
Thr Cys Val Ala Gln Asn Leu Val Gly	Ala Asp Thr Lys Thr Val	
500	505	510
Ser Val Val Val Gly Arg Ala Leu Leu	Gln Pro Gly Arg Asp Glu	
515	520	525
Gly Gln Gly Leu Glu Leu Arg Val Gln	Glu Thr His Pro Tyr His	
530	535	540
Ile Leu Leu Ser Trp Val Thr Pro Pro	Asn Thr Val Ser Thr Asn	
545	550	555
Leu Thr Trp Ser Ser Ala Ser Ser Leu	Arg Gly Gln Gly Ala Thr	
560	565	570
Ala Leu Ala Arg Leu Pro Arg Gly Thr	His Ser Tyr Asn Ile Thr	
575	580	585
Arg Leu Leu Gln Ala Thr Glu Tyr Trp	Ala Cys Leu Gln Val Ala	
590	595	600
Phe Ala Asp Ala His Thr Gln Leu Ala	Cys Val Trp Ala Arg Thr	
605	610	615
Lys Glu Ala Thr Ser Cys His Arg Ala	Leu Gly Asp Arg Pro Gly	
620	625	630
Leu Ile Ala Ile Leu Ala Leu Ala Val	Leu Leu Leu Ala Ala Gly	
635	640	645
Leu Ala Ala His Leu Gly Thr Gly Gln	Pro Arg Lys Gly Val Gly	
650	655	660
Gly Arg Arg Pro Leu Pro Pro Ala Trp	Ala Phe Trp Gly Trp Ser	
665	670	675

Ala Pro Ser Val Arg Val Val Ser Ala Pro Leu Val Leu Pro Trp  
                                 680                                685                                690

Asn Pro Gly Arg Lys Leu Pro Arg Ser Ser Glu Gly Glu Thr Leu  
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Leu Pro Pro Leu Ser Gln Asn Ser  
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<210> 246

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 246

aacaaggtaa gatgcatcc tg 22

<210> 247

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 247

aaacttgctg atggagacca gctc 24

<210> 248

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 248

aggggctgca aagcctggag agcctctcct tctatgacaa ccagc 45

<210> 249

<211> 3401

<212> DNA

<213> Homo Sapien

<400> 249

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catcaagttc gacgtggact gcaccgtgga cattgagagc ctgacgggct 200  
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<210> 250

<211> 546

<212> PRT

<213> Homo Sapien

<400> 250

Met	Arg	Gln	Thr	Ile	Ile	Lys	Val	Ile	Lys	Phe	Ile	Leu	Ile	Ile	1	5	10	15
Cys	Tyr	Thr	Val	Tyr	Tyr	Val	His	Asn	Ile	Lys	Phe	Asp	Val	Asp	20	25	30	
Cys	Thr	Val	Asp	Ile	Glu	Ser	Leu	Thr	Gly	Tyr	Arg	Thr	Tyr	Arg	35	40	45	
Cys	Ala	His	Pro	Leu	Ala	Thr	Leu	Phe	Lys	Ile	Leu	Ala	Ser	Phe	50	55	60	
Tyr	Ile	Ser	Leu	Val	Ile	Phe	Tyr	Gly	Leu	Ile	Cys	Met	Tyr	Thr	65	70	75	
Leu	Trp	Trp	Met	Leu	Arg	Arg	Ser	Leu	Lys	Lys	Tyr	Ser	Phe	Glu	80	85	90	
Ser	Ile	Arg	Glu	Glu	Ser	Ser	Tyr	Ser	Asp	Ile	Pro	Asp	Val	Lys				

	95	100	105
Asn Asp Phe Ala Phe Met Leu His Leu Ile Asp Gln Tyr Asp Pro			
	110	115	120
Leu Tyr Ser Lys Arg Phe Ala Val Phe Leu Ser Glu Val Ser Glu			
	125	130	135
Asn Lys Leu Arg Gln Leu Asn Leu Asn Asn Glu Trp Thr Leu Asp			
	140	145	150
Lys Leu Arg Gln Arg Leu Thr Lys Asn Ala Gln Asp Lys Leu Glu			
	155	160	165
Leu His Leu Phe Met Leu Ser Gly Ile Pro Asp Thr Val Phe Asp			
	170	175	180
Leu Val Glu Leu Glu Val Leu Lys Leu Glu Leu Ile Pro Asp Val			
	185	190	195
Thr Ile Pro Pro Ser Ile Ala Gln Leu Thr Gly Leu Lys Glu Leu			
	200	205	210
Trp Leu Tyr His Thr Ala Ala Lys Ile Glu Ala Pro Ala Leu Ala			
	215	220	225
Phe Leu Arg Glu Asn Leu Arg Ala Leu His Ile Lys Phe Thr Asp			
	230	235	240
Ile Lys Glu Ile Pro Leu Trp Ile Tyr Ser Leu Lys Thr Leu Glu			
	245	250	255
Glu Leu His Leu Thr Gly Asn Leu Ser Ala Glu Asn Asn Arg Tyr			
	260	265	270
Ile Val Ile Asp Gly Leu Arg Glu Leu Lys Arg Leu Lys Val Leu			
	275	280	285
Arg Leu Lys Ser Asn Leu Ser Lys Leu Pro Gln Val Val Thr Asp			
	290	295	300
Val Gly Val His Leu Gln Lys Leu Ser Ile Asn Asn Glu Gly Thr			
	305	310	315
Lys Leu Ile Val Leu Asn Ser Leu Lys Lys Met Ala Asn Leu Thr			
	320	325	330
Glu Leu Glu Leu Ile Arg Cys Asp Leu Glu Arg Ile Pro His Ser			
	335	340	345
Ile Phe Ser Leu His Asn Leu Gln Glu Ile Asp Leu Lys Asp Asn			
	350	355	360

Asn	Leu	Lys	Thr	Ile	Glu	Glu	Ile	Ile	Ser	Phe	Gln	His	Leu	His
				365					370					375
Arg	Leu	Thr	Cys	Leu	Lys	Leu	Trp	Tyr	Asn	His	Ile	Ala	Tyr	Ile
				380					385					390
Pro	Ile	Gln	Ile	Gly	Asn	Leu	Thr	Asn	Leu	Glu	Arg	Leu	Tyr	Leu
				395					400					405
Asn	Arg	Asn	Lys	Ile	Glu	Lys	Ile	Pro	Thr	Gln	Leu	Phe	Tyr	Cys
				410					415					420
Arg	Lys	Leu	Arg	Tyr	Leu	Asp	Leu	Ser	His	Asn	Asn	Leu	Thr	Phe
				425					430					435
Leu	Pro	Ala	Asp	Ile	Gly	Leu	Leu	Gln	Asn	Leu	Gln	Asn	Leu	Ala
				440					445					450
Ile	Thr	Ala	Asn	Arg	Ile	Glu	Thr	Leu	Pro	Pro	Glu	Leu	Phe	Gln
				455					460					465
Cys	Arg	Lys	Leu	Arg	Ala	Leu	His	Leu	Gly	Asn	Asn	Val	Leu	Gln
				470					475					480
Ser	Leu	Pro	Ser	Arg	Val	Gly	Glu	Leu	Thr	Asn	Leu	Thr	Gln	Ile
				485					490					495
Glu	Leu	Arg	Gly	Asn	Arg	Leu	Glu	Cys	Leu	Pro	Val	Glu	Leu	Gly
				500					505					510
Glu	Cys	Pro	Leu	Leu	Lys	Arg	Ser	Gly	Leu	Val	Val	Glu	Glu	Asp
				515					520					525
Leu	Phe	Asn	Thr	Leu	Pro	Pro	Glu	Val	Lys	Glu	Arg	Leu	Trp	Arg
				530					535					540
Ala	Asp	Lys	Glu	Gln	Ala									
				545										

&lt;210&gt; 251

&lt;211&gt; 20

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 251

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&lt;210&gt; 252

&lt;211&gt; 24

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 252  
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<210> 253  
<211> 47  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 253  
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<210> 254  
<211> 1650  
<212> DNA  
<213> Homo Sapien

<400> 254  
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&lt;210&gt; 255

&lt;211&gt; 452

&lt;212&gt; PRT

&lt;213&gt; Homo Sapien

&lt;400&gt; 255

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Leu	Leu	Pro	Leu	Leu	Leu	Gly	Leu	Asn	Ala	Gly	Ala	Val	Ile	Asp
			20						25				30	
Trp	Pro	Thr	Glu	Glu	Gly	Lys	Glu	Val	Trp	Asp	Tyr	Val	Thr	Val
			35					40					45	

Arg Lys Asp Ala Tyr Met Phe Trp Trp Leu Tyr Tyr Ala Thr Asn	50	55	60
Ser Cys Lys Asn Phe Ser Glu Leu Pro Leu Val Met Trp Leu Gln	65	70	75
Gly Gly Pro Gly Gly Ser Ser Thr Gly Phe Gly Asn Phe Glu Glu	80	85	90
Ile Gly Pro Leu Asp Ser Asp Leu Lys Pro Arg Lys Thr Thr Trp	95	100	105
Leu Gln Ala Ala Ser Leu Leu Phe Val Asp Asn Pro Val Gly Thr	110	115	120
Gly Phe Ser Tyr Val Asn Gly Ser Gly Ala Tyr Ala Lys Asp Leu	125	130	135
Ala Met Val Ala Ser Asp Met Met Val Leu Leu Lys Thr Phe Phe	140	145	150
Ser Cys His Lys Glu Phe Gln Thr Val Pro Phe Tyr Ile Phe Ser	155	160	165
Glu Ser Tyr Gly Gly Lys Met Ala Ala Gly Ile Gly Leu Glu Leu	170	175	180
Tyr Lys Ala Ile Gln Arg Gly Thr Ile Lys Cys Asn Phe Ala Gly	185	190	195
Val Ala Leu Gly Asp Ser Trp Ile Ser Pro Val Asp Ser Val Leu	200	205	210
Ser Trp Gly Pro Tyr Leu Tyr Ser Met Ser Leu Leu Glu Asp Lys	215	220	225
Gly Leu Ala Glu Val Ser Lys Val Ala Glu Gln Val Leu Asn Ala	230	235	240
Val Asn Lys Gly Leu Tyr Arg Glu Ala Thr Glu Leu Trp Gly Lys	245	250	255
Ala Glu Met Ile Ile Glu Gln Asn Thr Asp Gly Val Asn Phe Tyr	260	265	270
Asn Ile Leu Thr Lys Ser Thr Pro Thr Ser Thr Met Glu Ser Ser	275	280	285
Leu Glu Phe Thr Gln Ser His Leu Val Cys Leu Cys Gln Arg His	290	295	300
Val Arg His Leu Gln Arg Asp Ala Leu Ser Gln Leu Met Asn Gly			

305	310	315
Pro Ile Arg Lys Lys Leu Lys Ile Ile	Pro Glu Asp Gln Ser Trp	
320	325	330
Gly Gly Gln Ala Thr Asn Val Phe Val	Asn Met Glu Glu Asp Phe	
335	340	345
Met Lys Pro Val Ile Ser Ile Val Asp	Glu Leu Leu Glu Ala Gly	
350	355	360
Ile Asn Val Thr Val Tyr Asn Gly Gln	Leu Asp Leu Ile Val Asp	
365	370	375
Thr Met Gly Gln Glu Ala Trp Val Arg	Lys Leu Lys Trp Pro Glu	
380	385	390
Leu Pro Lys Phe Ser Gln Leu Lys Trp	Lys Ala Leu Tyr Ser Asp	
395	400	405
Pro Lys Ser Leu Glu Thr Ser Ala Phe	Val Lys Ser Tyr Lys Asn	
410	415	420
Leu Ala Phe Tyr Trp Ile Leu Lys Ala	Gly His Met Val Pro Ser	
425	430	435
Asp Gln Gly Asp Met Ala Leu Lys Met	Met Arg Leu Val Thr Gln	
440	445	450

Gln Glu

&lt;210&gt; 256

&lt;211&gt; 1100

&lt;212&gt; DNA

&lt;213&gt; Homo Sapien

&lt;400&gt; 256

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cgggtggatg gtccagtttg gccagctgac ttccatgcca tccttctgga 350
gcctgcaggc ctactacacc cgttacttcg tatcgaatat ctatctgagc 400

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100

100

1000

Ser Asp Pro Ser Gly Trp Met Val Gln Phe Gly Gln Leu Thr Ser  
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 Met Pro Ser Phe Trp Ser Leu Gln Ala Tyr Tyr Thr Arg Tyr Phe  
 110 115 120  
 Val Ser Asn Ile Tyr Leu Ser Pro Arg Tyr Leu Gly Asn Ser Pro  
 125 130 135  
 Tyr Asp Ile Ala Leu Val Lys Leu Ser Ala Pro Val Thr Tyr Thr  
 140 145 150  
 Lys His Ile Gln Pro Ile Cys Leu Gln Ala Ser Thr Phe Glu Phe  
 155 160 165  
 Glu Asn Arg Thr Asp Cys Trp Val Thr Gly Trp Gly Tyr Ile Lys  
 170 175 180  
 Glu Asp Glu Ala Leu Pro Ser Pro His Thr Leu Gln Glu Val Gln  
 185 190 195  
 Val Ala Ile Ile Asn Asn Ser Met Cys Asn His Leu Phe Leu Lys  
 200 205 210  
 Tyr Ser Phe Arg Lys Asp Ile Phe Gly Asp Met Val Cys Ala Gly  
 215 220 225  
 Asn Ala Gln Gly Gly Lys Asp Ala Cys Phe Gly Asp Ser Gly Gly  
 230 235 240  
 Pro Leu Ala Cys Asn Lys Asn Gly Leu Trp Tyr Gln Ile Gly Val  
 245 250 255  
 Val Ser Trp Gly Val Gly Cys Gly Arg Pro Asn Arg Pro Gly Val  
 260 265 270  
 Tyr Thr Asn Ile Ser His His Phe Glu Trp Ile Gln Lys Leu Met  
 275 280 285  
 Ala Gln Ser Gly Met Ser Gln Pro Asp Pro Ser Trp Pro Leu Leu  
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 Phe Phe Pro Leu Leu Trp Ala Leu Pro Leu Leu Gly Pro Val  
 305 310

&lt;210&gt; 258

&lt;211&gt; 2427

&lt;212&gt; DNA

&lt;213&gt; Homo Sapien

&lt;400&gt; 258

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 tgtagatttt tgctcttctc agtttactca ttgtccctg gaacaaatca 2350  
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<210> 259

<211> 556

<212> PRT

<213> Homo Sapien

<400> 259

Met	Gly	Leu	Gln	Ala	Cys	Leu	Leu	Gly	Leu	Phe	Ala	Leu	Ile	Leu
1					5				10				15	

Ser Gly Lys Cys Ser Tyr Ser Pro Glu Pro Asp Gln Arg Arg Thr

20	25	30
Leu Pro Pro Gly Trp Val Ser Leu Gly Arg Ala Asp Pro Glu Glu 35 40 45		
Glu Leu Ser Leu Thr Phe Ala Leu Arg Gln Gln Asn Val Glu Arg 50 55 60		
Leu Ser Glu Leu Val Gln Ala Val Ser Asp Pro Ser Ser Pro Gln 65 70 75		
Tyr Gly Lys Tyr Leu Thr Leu Glu Asn Val Ala Asp Leu Val Arg 80 85 90		
Pro Ser Pro Leu Thr Leu His Thr Val Gln Lys Trp Leu Leu Ala 95 100 105		
Ala Gly Ala Gln Lys Cys His Ser Val Ile Thr Gln Asp Phe Leu 110 115 120		
Thr Cys Trp Leu Ser Ile Arg Gln Ala Glu Leu Leu Leu Pro Gly 125 130 135		
Ala Glu Phe His His Tyr Val Gly Gly Pro Thr Glu Thr His Val 140 145 150		
Val Arg Ser Pro His Pro Tyr Gln Leu Pro Gln Ala Leu Ala Pro 155 160 165		
His Val Asp Phe Val Gly Gly Leu His Arg Phe Pro Pro Thr Ser 170 175 180		
Ser Leu Arg Gln Arg Pro Glu Pro Gln Val Thr Gly Thr Val Gly 185 190 195		
Leu His Leu Gly Val Thr Pro Ser Val Ile Arg Lys Arg Tyr Asn 200 205 210		
Leu Thr Ser Gln Asp Val Gly Ser Gly Thr Ser Asn Asn Ser Gln 215 220 225		
Ala Cys Ala Gln Phe Leu Glu Gln Tyr Phe His Asp Ser Asp Leu 230 235 240		
Ala Gln Phe Met Arg Leu Phe Gly Gly Asn Phe Ala His Gln Ala 245 250 255		
Ser Val Ala Arg Val Val Gly Gln Gln Gly Arg Gly Arg Ala Gly 260 265 270		
Ile Glu Ala Ser Leu Asp Val Gln Tyr Leu Met Ser Ala Gly Ala 275 280 285		

Asn Ile Ser Thr Trp Val Tyr Ser Ser	Pro Gly Arg His Glu Gly	290	295	300
Gln Glu Pro Phe Leu Gln Trp Leu Met	Leu Leu Ser Asn Glu Ser	305	310	315
Ala Leu Pro His Val His Thr Val Ser	Tyr Gly Asp Asp Glu Asp	320	325	330
Ser Leu Ser Ser Ala Tyr Ile Gln Arg	Val Asn Thr Glu Leu Met	335	340	345
Lys Ala Ala Ala Arg Gly Leu Thr Leu	Leu Phe Ala Ser Gly Asp	350	355	360
Ser Gly Ala Gly Cys Trp Ser Val Ser	Gly Arg His Gln Phe Arg	365	370	375
Pro Thr Phe Pro Ala Ser Ser Pro Tyr	Val Thr Thr Val Gly Gly	380	385	390
Thr Ser Phe Gln Glu Pro Phe Leu Ile	Thr Asn Glu Ile Val Asp	395	400	405
Tyr Ile Ser Gly Gly Gly Phe Ser Asn	Val Phe Pro Arg Pro Ser	410	415	420
Tyr Gln Glu Glu Ala Val Thr Lys Phe	Leu Ser Ser Ser Pro His	425	430	435
Leu Pro Pro Ser Ser Tyr Phe Asn Ala	Ser Gly Arg Ala Tyr Pro	440	445	450
Asp Val Ala Ala Leu Ser Asp Gly Tyr	Trp Val Val Ser Asn Arg	455	460	465
Val Pro Ile Pro Trp Val Ser Gly Thr	Ser Ala Ser Thr Pro Val	470	475	480
Phe Gly Gly Ile Leu Ser Leu Ile Asn	Glu His Arg Ile Leu Ser	485	490	495
Gly Arg Pro Pro Leu Gly Phe Leu Asn	Pro Arg Leu Tyr Gln Gln	500	505	510
His Gly Ala Gly Leu Phe Asp Val Thr	Arg Gly Cys His Glu Ser	515	520	525
Cys Leu Asp Glu Glu Val Glu Gly Gln	Gly Phe Cys Ser Gly Pro	530	535	540
Gly Trp Asp Pro Val Thr Gly Trp Gly	Thr Pro Thr Ser Gln Leu	545	550	555

Cys

&lt;210&gt; 260

&lt;211&gt; 1638

&lt;212&gt; DNA

&lt;213&gt; Homo Sapien

&lt;400&gt; 260

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 cgcgccccgg gcgggctgct cggcgcgga cagtgtctcg catggcaggg 100  
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<210> 261

<211> 383

<212> PRT

<213> Homo Sapien

<400> 261

Met	Ala	Gly	Ile	Pro	Gly	Leu	Leu	Phe	Leu	Leu	Phe	Phe	Leu	Leu
1				5				10					15	

Cys	Ala	Val	Gly	Gln	Val	Ser	Pro	Tyr	Ser	Ala	Pro	Trp	Lys	Pro
			20					25					30	

Thr	Trp	Pro	Ala	Tyr	Arg	Leu	Pro	Val	Val	Leu	Pro	Gln	Ser	Thr
			35					40					45	

Leu	Asn	Leu	Ala	Lys	Pro	Asp	Phe	Gly	Ala	Glu	Ala	Lys	Leu	Glu
			50					55					60	

Val	Ser	Ser	Ser	Cys	Gly	Pro	Gln	Cys	His	Lys	Gly	Thr	Pro	Leu
			65					70					75	

Pro	Thr	Tyr	Glu	Glu	Ala	Lys	Gln	Tyr	Leu	Ser	Tyr	Glu	Thr	Leu
			80					85					90	

Tyr	Ala	Asn	Gly	Ser	Arg	Thr	Glu	Thr	Gln	Val	Gly	Ile	Tyr	Ile
			95						100				105	

Leu	Ser	Ser	Ser	Gly	Asp	Gly	Ala	Gln	His	Arg	Asp	Ser	Gly	Ser
			110					115					120	



Ser Gly Lys Ser Arg Arg Lys Arg Gln Ile Tyr Gly Tyr Asp Ser	125	130	135
Arg Phe Ser Ile Phe Gly Lys Asp Phe Leu Leu Asn Tyr Pro Phe	140	145	150
Ser Thr Ser Val Lys Leu Ser Thr Gly Cys Thr Gly Thr Leu Val	155	160	165
Ala Glu Lys His Val Leu Thr Ala Ala His Cys Ile His Asp Gly	170	175	180
Lys Thr Tyr Val Lys Gly Thr Gln Lys Leu Arg Val Gly Phe Leu	185	190	195
Lys Pro Lys Phe Lys Asp Gly Gly Arg Gly Ala Asn Asp Ser Thr	200	205	210
Ser Ala Met Pro Glu Gln Met Lys Phe Gln Trp Ile Arg Val Lys	215	220	225
Arg Thr His Val Pro Lys Gly Trp Ile Lys Gly Asn Ala Asn Asp	230	235	240
Ile Gly Met Asp Tyr Asp Tyr Ala Leu Leu Glu Leu Lys Lys Pro	245	250	255
His Lys Arg Lys Phe Met Lys Ile Gly Val Ser Pro Pro Ala Lys	260	265	270
Gln Leu Pro Gly Gly Arg Ile His Phe Ser Gly Tyr Asp Asn Asp	275	280	285
Arg Pro Gly Asn Leu Val Tyr Arg Phe Cys Asp Val Lys Asp Glu	290	295	300
Thr Tyr Asp Leu Leu Tyr Gln Gln Cys Asp Ala Gln Pro Gly Ala	305	310	315
Ser Gly Ser Gly Val Tyr Val Arg Met Trp Lys Arg Gln Gln Gln	320	325	330
Lys Trp Glu Arg Lys Ile Ile Gly Ile Phe Ser Gly His Gln Trp	335	340	345
Val Asp Met Asn Gly Ser Pro Gln Asp Phe Asn Val Ala Val Arg	350	355	360
Ile Thr Pro Leu Lys Tyr Ala Gln Ile Cys Tyr Trp Ile Lys Gly	365	370	375
Asn Tyr Leu Asp Cys Arg Glu Gly	380		

<210> 262  
<211> 1378  
<212> DNA  
<213> Homo Sapien

<400> 262  
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caggatacct gttccccag cctgtgggaa gccccagcag ctgaaccggg 200  
ttgtgggcgg cgaggacagc actgacagcg agtggccctg gatcgtgagc 250  
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<210> 263

<211> 317

<212> PRT

<213> Homo Sapien

<400> 263

Met	Val	Val	Ser	Gly	Ala	Pro	Pro	Ala	Leu	Gly	Gly	Gly	Cys	Leu	1	5	10	15
Gly	Thr	Phe	Thr	Ser	Leu	Leu	Leu	Leu	Ala	Ser	Thr	Ala	Ile	Leu	20	25	30	
Asn	Ala	Ala	Arg	Ile	Pro	Val	Pro	Pro	Ala	Cys	Gly	Lys	Pro	Gln	35	40	45	
Gln	Leu	Asn	Arg	Val	Val	Gly	Gly	Glu	Asp	Ser	Thr	Asp	Ser	Glu	50	55	60	
Trp	Pro	Trp	Ile	Val	Ser	Ile	Gln	Lys	Asn	Gly	Thr	His	His	Cys	65	70	75	
Ala	Gly	Ser	Leu	Leu	Thr	Ser	Arg	Trp	Val	Ile	Thr	Ala	Ala	His	80	85	90	
Cys	Phe	Lys	Asp	Asn	Leu	Asn	Lys	Pro	Tyr	Leu	Phe	Ser	Val	Leu	95	100	105	
Leu	Gly	Ala	Trp	Gln	Leu	Gly	Asn	Pro	Gly	Ser	Arg	Ser	Gln	Lys	110	115	120	
Val	Gly	Val	Ala	Trp	Val	Glu	Pro	His	Pro	Val	Tyr	Ser	Trp	Lys	125	130	135	
Glu	Gly	Ala	Cys	Ala	Asp	Ile	Ala	Leu	Val	Arg	Leu	Glu	Arg	Ser	140	145	150	
Ile	Gln	Phe	Ser	Glu	Arg	Val	Leu	Pro	Ile	Cys	Leu	Pro	Asp	Ala	155	160	165	
Ser	Ile	His	Leu	Pro	Pro	Asn	Thr	His	Cys	Trp	Ile	Ser	Gly	Trp	170	175	180	

Gly	Ser	Ile	Gln	Asp	Gly	Val	Pro	Leu	Pro	His	Pro	Gln	Thr	Leu
				185					190					195
Gln	Lys	Leu	Lys	Val	Pro	Ile	Ile	Asp	Ser	Glu	Val	Cys	Ser	His
				200					205					210
Leu	Tyr	Trp	Arg	Gly	Ala	Gly	Gln	Gly	Pro	Ile	Thr	Glu	Asp	Met
				215					220					225
Leu	Cys	Ala	Gly	Tyr	Leu	Glu	Gly	Glu	Arg	Asp	Ala	Cys	Leu	Gly
				230					235					240
Asp	Ser	Gly	Gly	Pro	Leu	Met	Cys	Gln	Val	Asp	Gly	Ala	Trp	Leu
				245					250					255
Leu	Ala	Gly	Ile	Ile	Ser	Trp	Gly	Glu	Gly	Cys	Ala	Glu	Arg	Asn
				260					265					270
Arg	Pro	Gly	Val	Tyr	Ile	Ser	Leu	Ser	Ala	His	Arg	Ser	Trp	Val
				275					280					285
Glu	Lys	Ile	Val	Gln	Gly	Val	Gln	Leu	Arg	Gly	Arg	Ala	Gln	Gly
				290					295					300
Gly	Gly	Ala	Leu	Arg	Ala	Pro	Ser	Gln	Gly	Ser	Gly	Ala	Ala	Ala
				305					310					315

Arg Ser

<210> 264

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 264

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<210> 265

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 265

gcagaggtgt ctaagggttg 19

<210> 266

<211> 24

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 266  
agctctagac caatgccagc ttcc 24

<210> 267  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 267  
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<210> 268  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 268  
ggggaattca ccctatgaca ttgcc 25

<210> 269  
<211> 24  
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<400> 269  
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<210> 270  
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<210> 271  
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<210> 276  
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<210> 277  
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<400> 277  
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<210> 278  
<211> 18  
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<400> 278  
tgacaatgac cgaccagg 18

<210> 279  
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<400> 279  
gcatgcatt gctggtagag caag 24

<210> 280  
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<212> DNA  
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<400> 280

ttacagtgcc ccctggaaac ccacttggcc tgcataccgc ctccc 45

<210> 281

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 281

cgtctcgagc gctccatata gttcccttgc ccca 34

<210> 282

<211> 61

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 282

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tgccaggtgg a 61

<210> 283

<211> 119

<212> DNA

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<220>

<223> Synthetic Oligonucleotide Probe

<400> 283

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atgctgtgtg ccggctact 119

<210> 284

<211> 1875

<212> DNA

<213> Homo Sapien

<400> 284

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ccgctactgc tactgctggt ggccaccaca ggccccgttg gagccctcac 100



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 ataaaaacct gtccaacctg tgaaa 1875

<210> 285

<211> 463

<212> PRT

<213> Homo Sapien

<400> 285

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			20						25				30		
Glu	Glu	Lys	Arg	Leu	Met	Val	Glu	Leu	His	Asn	Leu	Tyr	Arg	Ala	
			35						40				45		
Gln	Val	Ser	Pro	Thr	Ala	Ser	Asp	Met	Leu	His	Met	Arg	Trp	Asp	
			50						55				60		
Glu	Glu	Leu	Ala	Ala	Phe	Ala	Lys	Ala	Tyr	Ala	Arg	Gln	Cys	Val	
			65						70				75		
Trp	Gly	His	Asn	Lys	Glu	Arg	Gly	Arg	Arg	Gly	Glu	Asn	Leu	Phe	
			80						85				90		
Ala	Ile	Thr	Asp	Glu	Gly	Met	Asp	Val	Pro	Leu	Ala	Met	Glu	Glu	
			95						100				105		
Trp	His	His	Glu	Arg	Glu	His	Tyr	Asn	Leu	Ser	Ala	Ala	Thr	Cys	
			110						115				120		
Ser	Pro	Gly	Gln	Met	Cys	Gly	His	Tyr	Thr	Gln	Val	Val	Trp	Ala	
			125						130				135		

Lys Thr Glu Arg	Ile Gly Cys Gly Ser	His Phe Cys Glu Lys Leu
140	145	150
Gln Gly Val Glu	Glu Thr Asn Ile Glu	Leu Leu Val Cys Asn Tyr
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Glu Pro Pro Gly	Asn Val Lys Gly Lys	Arg Pro Tyr Gln Glu Gly
170	175	180
Thr Pro Cys Ser	Gln Cys Pro Ser Gly	Tyr His Cys Lys Asn Ser
185	190	195
Leu Cys Glu Pro	Ile Gly Ser Pro Glu	Asp Ala Gln Asp Leu Pro
200	205	210
Tyr Leu Val Thr	Glu Ala Pro Ser Phe	Arg Ala Thr Glu Ala Ser
215	220	225
Asp Ser Arg Lys	Met Gly Thr Pro Ser	Ser Leu Ala Thr Gly Ile
230	235	240
Pro Ala Phe Leu	Val Thr Glu Val Ser	Gly Ser Leu Ala Thr Lys
245	250	255
Ala Leu Pro Ala	Val Glu Thr Gln Ala	Pro Thr Ser Leu Ala Thr
260	265	270
Lys Asp Pro Pro	Ser Met Ala Thr Glu	Ala Pro Pro Cys Val Thr
275	280	285
Thr Glu Val Pro	Ser Ile Leu Ala Ala	His Ser Leu Pro Ser Leu
290	295	300
Asp Glu Glu Pro	Val Thr Phe Pro Lys	Ser Thr His Val Pro Ile
305	310	315
Pro Lys Ser Ala	Asp Lys Val Thr Asp	Lys Thr Lys Val Pro Ser
320	325	330
Arg Ser Pro Glu	Asn Ser Leu Asp Pro	Lys Met Ser Leu Thr Gly
335	340	345
Ala Arg Glu Leu	Leu Pro His Ala Gln	Glu Glu Ala Glu Ala Glu
350	355	360
Ala Glu Leu Pro	Pro Ser Ser Glu Val	Leu Ala Ser Val Phe Pro
365	370	375
Ala Gln Asp Lys	Pro Gly Glu Leu Gln	Ala Thr Leu Asp His Thr
380	385	390
Gly His Thr Ser	Ser Lys Ser Leu Pro	Asn Phe Pro Asn Thr Ser
395	400	405

Ala Thr Ala Asn Ala Thr Gly Gly Arg Ala Leu Ala Leu Gln Ser  
 410 415 420

Ser Leu Pro Gly Ala Glu Gly Pro Asp Lys Pro Ser Val Val Ser  
 425 430 435

Gly Leu Asn Ser Gly Pro Gly His Val Trp Gly Pro Leu Leu Gly  
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Leu Leu Leu Leu Pro Pro Leu Val Leu Ala Gly Ile Phe  
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<210> 286

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 286

tcctgcagtt tcctgatgc 19

<210> 287

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 287

ctcatattgc acaccagtaa ttcg 24

<210> 288

<211> 45

<212> DNA

<213> Artificial Sequence

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<223> Synthetic Oligonucleotide Probe

<400> 288

atgaggagaa acgtttgatg gtggagctgc acaacctcta ccggg 45

<210> 289

<211> 3662

<212> DNA

<213> Homo Sapien

<400> 289

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<211> 1059

<212> PRT

<213> Homo Sapien

<400> 290

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Ala	Asn	Ile	Thr	Leu	Leu	Ser	Leu	Ala	Gly	Asn	Arg	Ile	Val	Glu	65	70	75
Ile	Leu	Pro	Glu	His	Leu	Lys	Glu	Phe	Gln	Ser	Leu	Glu	Thr	Leu	80	85	90
Asp	Leu	Ser	Ser	Asn	Asn	Ile	Ser	Glu	Leu	Gln	Thr	Ala	Phe	Pro	95	100	105
Ala	Leu	Gln	Leu	Lys	Tyr	Leu	Tyr	Leu	Asn	Ser	Asn	Arg	Val	Thr	110	115	120
Ser	Met	Glu	Pro	Gly	Tyr	Phe	Asp	Asn	Leu	Ala	Asn	Thr	Leu	Leu	125	130	135
Val	Leu	Lys	Leu	Asn	Arg	Asn	Arg	Ile	Ser	Ala	Ile	Pro	Pro	Lys	140	145	150
Met	Phe	Lys	Leu	Pro	Gln	Leu	Gln	His	Leu	Glu	Leu	Asn	Arg	Asn	155	160	165
Lys	Ile	Lys	Asn	Val	Asp	Gly	Leu	Thr	Phe	Gln	Gly	Leu	Gly	Ala	170	175	180
Leu	Lys	Ser	Leu	Lys	Met	Gln	Arg	Asn	Gly	Val	Thr	Lys	Leu	Met	185	190	195
Asp	Gly	Ala	Phe	Trp	Gly	Leu	Ser	Asn	Met	Glu	Ile	Leu	Gln	Leu	200	205	210
Asp	His	Asn	Asn	Leu	Thr	Glu	Ile	Thr	Lys	Gly	Trp	Leu	Tyr	Gly	215	220	225
Leu	Leu	Met	Leu	Gln	Glu	Leu	His	Leu	Ser	Gln	Asn	Ala	Ile	Asn	230	235	240
Arg	Ile	Ser	Pro	Asp	Ala	Trp	Glu	Phe	Cys	Gln	Lys	Leu	Ser	Glu	245	250	255
Leu	Asp	Leu	Thr	Phe	Asn	His	Leu	Ser	Arg	Leu	Asp	Asp	Ser	Ser	260	265	270
Phe	Leu	Gly	Leu	Ser	Leu	Leu	Asn	Thr	Leu	His	Ile	Gly	Asn	Asn	275	280	285
Arg	Val	Ser	Tyr	Ile	Ala	Asp	Cys	Ala	Phe	Arg	Gly	Leu	Ser	Ser			



290										295					300				
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Glu	Asp	Met	Asn	Gly	Ala	Phe	Ser	Gly	Leu	Asp	Lys	Leu	Arg	Arg					
				320					325					330					
Leu	Ile	Leu	Gln	Gly	Asn	Arg	Ile	Arg	Ser	Ile	Thr	Lys	Lys	Ala					
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Phe	Thr	Gly	Leu	Asp	Ala	Leu	Glu	His	Leu	Asp	Leu	Ser	Asp	Asn					
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Ala	Ile	Met	Ser	Leu	Gln	Gly	Asn	Ala	Phe	Ser	Gln	Met	Lys	Lys					
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Gln	Leu	Lys	Trp	Leu	Pro	Gln	Trp	Val	Ala	Glu	Asn	Asn	Phe	Gln					
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Ser	Phe	Val	Asn	Ala	Ser	Cys	Ala	His	Pro	Gln	Leu	Leu	Lys	Gly					
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Arg	Ser	Ile	Phe	Ala	Val	Ser	Pro	Asp	Gly	Phe	Val	Cys	Asp	Asp					
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Phe	Pro	Lys	Pro	Gln	Ile	Thr	Val	Gln	Pro	Glu	Thr	Gln	Ser	Ala					
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Ile	Lys	Gly	Ser	Asn	Leu	Ser	Phe	Ile	Cys	Ser	Ala	Ala	Ser	Ser					
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Ser	Asp	Ser	Pro	Met	Thr	Phe	Ala	Trp	Lys	Lys	Asp	Asn	Glu	Leu					
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Leu	His	Asp	Ala	Glu	Met	Glu	Asn	Tyr	Ala	His	Leu	Arg	Ala	Gln					
				485					490					495					
Gly	Gly	Glu	Val	Met	Glu	Tyr	Thr	Thr	Ile	Leu	Arg	Leu	Arg	Glu					
				500					505					510					
Val	Glu	Phe	Ala	Ser	Glu	Gly	Lys	Tyr	Gln	Cys	Val	Ile	Ser	Asn					
				515					520					525					
His	Phe	Gly	Ser	Ser	Tyr	Ser	Val	Lys	Ala	Lys	Leu	Thr	Val	Asn					
				530					535					540					
Met	Leu	Pro	Ser	Phe	Thr	Lys	Thr	Pro	Met	Asp	Leu	Thr	Ile	Arg					
				545					550					555					

Ala Gly Ala Met	Ala Arg Leu Glu Cys	Ala Ala Val Gly His	Pro
560	565		570
Ala Pro Gln Ile	Ala Trp Gln Lys Asp	Gly Gly Thr Asp Phe	Pro
575	580		585
Ala Ala Arg Glu	Arg Arg Met His Val	Met Pro Glu Asp Asp	Val
590	595		600
Phe Phe Ile Val	Asp Val Lys Ile Glu	Asp Ile Gly Val Tyr	Ser
605	610		615
Cys Thr Ala Gln	Asn Ser Ala Gly Ser	Ile Ser Ala Asn Ala	Thr
620	625		630
Leu Thr Val Leu	Glu Thr Pro Ser Phe	Leu Arg Pro Leu Leu	Asp
635	640		645
Arg Thr Val Thr	Lys Gly Glu Thr Ala	Val Leu Gln Cys Ile	Ala
650	655		660
Gly Gly Ser Pro	Pro Pro Lys Leu Asn	Trp Thr Lys Asp Asp	Ser
665	670		675
Pro Leu Val Val	Thr Glu Arg His Phe	Phe Ala Ala Gly Asn	Gln
680	685		690
Leu Leu Ile Ile	Val Asp Ser Asp Val	Ser Asp Ala Gly Lys	Tyr
695	700		705
Thr Cys Glu Met	Ser Asn Thr Leu Gly	Thr Glu Arg Gly Asn	Val
710	715		720
Arg Leu Ser Val	Ile Pro Thr Pro Thr	Cys Asp Ser Pro Gln	Met
725	730		735
Thr Ala Pro Ser	Leu Asp Asp Asp Gly	Trp Ala Thr Val Gly	Val
740	745		750
Val Ile Ile Ala	Val Val Cys Cys Val	Val Gly Thr Ser Leu	Val
755	760		765
Trp Val Val Ile	Ile Tyr His Thr Arg	Arg Arg Asn Glu Asp	Cys
770	775		780
Ser Ile Thr Asn	Thr Asp Glu Thr Asn	Leu Pro Ala Asp Ile	Pro
785	790		795
Ser Tyr Leu Ser	Ser Gln Gly Thr Leu	Ala Asp Arg Gln Asp	Gly
800	805		810

Tyr Val Ser Ser Glu Ser Gly Ser His	His Gln Phe Val Thr Ser
815	820 825
Ser Gly Ala Gly Phe Phe Leu Pro Gln His Asp Ser Ser Gly Thr	
830	835 840
Cys His Ile Asp Asn Ser Ser Glu Ala Asp Val Glu Ala Ala Thr	
845	850 855
Asp Leu Phe Leu Cys Pro Phe Leu Gly Ser Thr Gly Pro Met Tyr	
860	865 870
Leu Lys Gly Asn Val Tyr Gly Ser Asp Pro Phe Glu Thr Tyr His	
875	880 885
Thr Gly Cys Ser Pro Asp Pro Arg Thr Val Leu Met Asp His Tyr	
890	895 900
Glu Pro Ser Tyr Ile Lys Lys Lys Glu Cys Tyr Pro Cys Ser His	
905	910 915
Pro Ser Glu Glu Ser Cys Glu Arg Ser Phe Ser Asn Ile Ser Trp	
920	925 930
Pro Ser His Val Arg Lys Leu Leu Asn Thr Ser Tyr Ser His Asn	
935	940 945
Glu Gly Pro Gly Met Lys Asn Leu Cys Leu Asn Lys Ser Ser Leu	
950	955 960
Asp Phe Ser Ala Asn Pro Glu Pro Ala Ser Val Ala Ser Ser Asn	
965	970 975
Ser Phe Met Gly Thr Phe Gly Lys Ala Leu Arg Arg Pro His Leu	
980	985 990
Asp Ala Tyr Ser Ser Phe Gly Gln Pro Ser Asp Cys Gln Pro Arg	
995	1000 1005
Ala Phe Tyr Leu Lys Ala His Ser Ser Pro Asp Leu Asp Ser Gly	
1010	1015 1020
Ser Glu Glu Asp Gly Lys Glu Arg Thr Asp Phe Gln Glu Glu Asn	
1025	1030 1035
His Ile Cys Thr Phe Lys Gln Thr Leu Glu Asn Tyr Arg Thr Pro	
1040	1045 1050
Asn Phe Gln Ser Tyr Asp Leu Asp Thr	
1055	

&lt;210&gt; 291

&lt;211&gt; 2906

&lt;212&gt; DNA

&lt;213&gt; Homo Sapien

&lt;400&gt; 291

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tggaaccgaa cgcaatggat aaactgattg tgcaagagag aaggaagaac 150  
gaagcttttt cttgtgagcc ctggatctta acacaaatgt gtatatgtgc 200  
acacagggag cattcaagaa tgaaataaac cagagttaga cccgcggggg 250  
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gatatttttg gaatgaaaag tttggggctt ttttagtaaa gtaaagaact 450  
ggtgtggtgg tgttttcctt totttttgaa tttcccacia gaggagagga 500  
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tttgtgcta tgttgactaa aattgacgga taattgcagt tggatttttc 650  
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 tgactgggct aaatctactg tttcaaaaaa gtgtctttac aaaaaaaca 2850  
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 caaaaa 2906

<210> 292

<211> 640

<212> PRT

<213> Homo Sapien

<400> 292

Met	Leu	Asn	Lys	Met	Thr	Leu	His	Pro	Gln	Gln	Ile	Met	Ile	Gly
1				5					10					15

Pro	Arg	Phe	Asn	Arg	Ala	Leu	Phe	Asp	Pro	Leu	Leu	Val	Val	Leu
			20						25					30

Leu	Ala	Leu	Gln	Leu	Leu	Val	Val	Ala	Gly	Leu	Val	Arg	Ala	Gln
			35						40					45

Thr	Cys	Pro	Ser	Val	Cys	Ser	Cys	Ser	Asn	Gln	Phe	Ser	Lys	Val
				50					55					60

Ile	Cys	Val	Arg	Lys	Asn	Leu	Arg	Glu	Val	Pro	Asp	Gly	Ile	Ser
				65					70					75

Thr	Asn	Thr	Arg	Leu	Leu	Asn	Leu	His	Glu	Asn	Gln	Ile	Gln	Ile
				80					85					90

Ile	Lys	Val	Asn	Ser	Phe	Lys	His	Leu	Arg	His	Leu	Glu	Ile	Leu
				95					100					105

Gln	Leu	Ser	Arg	Asn	His	Ile	Arg	Thr	Ile	Glu	Ile	Gly	Ala	Phe
				110					115					120

Asn	Gly	Leu	Ala	Asn	Leu	Asn	Thr	Leu	Glu	Leu	Phe	Asp	Asn	Arg
				125					130					135

Leu	Thr	Thr	Ile	Pro	Asn	Gly	Ala	Phe	Val	Tyr	Leu	Ser	Lys	Leu
				140					145					150

Lys	Glu	Leu	Trp	Leu	Arg	Asn	Asn	Pro	Ile	Glu	Ser	Ile	Pro	Ser
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

155	160	165
Tyr Ala Phe Asn Arg Ile Pro Ser Leu	Arg Arg Leu Asp Leu Gly	
170	175	180
Glu Leu Lys Arg Leu Ser Tyr Ile Ser	Glu Gly Ala Phe Glu Gly	
185	190	195
Leu Ser Asn Leu Arg Tyr Leu Asn Leu	Ala Met Cys Asn Leu Arg	
200	205	210
Glu Ile Pro Asn Leu Thr Pro Leu Ile	Lys Leu Asp Glu Leu Asp	
215	220	225
Leu Ser Gly Asn His Leu Ser Ala Ile	Arg Pro Gly Ser Phe Gln	
230	235	240
Gly Leu Met His Leu Gln Lys Leu Trp	Met Ile Gln Ser Gln Ile	
245	250	255
Gln Val Ile Glu Arg Asn Ala Phe Asp	Asn Leu Gln Ser Leu Val	
260	265	270
Glu Ile Asn Leu Ala His Asn Asn Leu	Thr Leu Leu Pro His Asp	
275	280	285
Leu Phe Thr Pro Leu His His Leu Glu	Arg Ile His Leu His His	
290	295	300
Asn Pro Trp Asn Cys Asn Cys Asp Ile	Leu Trp Leu Ser Trp Trp	
305	310	315
Ile Lys Asp Met Ala Pro Ser Asn Thr	Ala Cys Cys Ala Arg Cys	
320	325	330
Asn Thr Pro Pro Asn Leu Lys Gly Arg	Tyr Ile Gly Glu Leu Asp	
335	340	345
Gln Asn Tyr Phe Thr Cys Tyr Ala Pro	Val Ile Val Glu Pro Pro	
350	355	360
Ala Asp Leu Asn Val Thr Glu Gly Met	Ala Ala Glu Leu Lys Cys	
365	370	375
Arg Ala Ser Thr Ser Leu Thr Ser Val	Ser Trp Ile Thr Pro Asn	
380	385	390
Gly Thr Val Met Thr His Gly Ala Tyr	Lys Val Arg Ile Ala Val	
395	400	405
Leu Ser Asp Gly Thr Leu Asn Phe Thr	Asn Val Thr Val Gln Asp	
410	415	420

Thr Gly Met Tyr Thr Cys Met Val Ser Asn Ser Val Gly Asn Thr  
 425 430 435  
 Thr Ala Ser Ala Thr Leu Asn Val Thr Ala Ala Thr Thr Thr Pro  
 440 445 450  
 Phe Ser Tyr Phe Ser Thr Val Thr Val Glu Thr Met Glu Pro Ser  
 455 460 465  
 Gln Asp Glu Ala Arg Thr Thr Asp Asn Asn Val Gly Pro Thr Pro  
 470 475 480  
 Val Val Asp Trp Glu Thr Thr Asn Val Thr Thr Ser Leu Thr Pro  
 485 490 495  
 Gln Ser Thr Arg Ser Thr Glu Lys Thr Phe Thr Ile Pro Val Thr  
 500 505 510  
 Asp Ile Asn Ser Gly Ile Pro Gly Ile Asp Glu Val Met Lys Thr  
 515 520 525  
 Thr Lys Ile Ile Ile Gly Cys Phe Val Ala Ile Thr Leu Met Ala  
 530 535 540  
 Ala Val Met Leu Val Ile Phe Tyr Lys Met Arg Lys Gln His His  
 545 550 555  
 Arg Gln Asn His His Ala Pro Thr Arg Thr Val Glu Ile Ile Asn  
 560 565 570  
 Val Asp Asp Glu Ile Thr Gly Asp Thr Pro Met Glu Ser His Leu  
 575 580 585  
 Pro Met Pro Ala Ile Glu His Glu His Leu Asn His Tyr Asn Ser  
 590 595 600  
 Tyr Lys Ser Pro Phe Asn His Thr Thr Thr Val Asn Thr Ile Asn  
 605 610 615  
 Ser Ile His Ser Ser Val His Glu Pro Leu Leu Ile Arg Met Asn  
 620 625 630  
 Ser Lys Asp Asn Val Gln Glu Thr Gln Ile  
 635 640

&lt;210&gt; 293

&lt;211&gt; 4053

&lt;212&gt; DNA

&lt;213&gt; Homo Sapien

&lt;400&gt; 293

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<210> 294

<211> 1119

<212> PRT

<213> Homo Sapien

<400> 294

Met Ser Ala Pro Ser Leu Arg Ala Arg Ala Ala Gly Leu Gly Leu  
1 5 10 15

Leu Leu Cys Ala Val Leu Gly Arg Ala Gly Arg Ser Asp Ser Gly  
20 25 30

Gly Arg Gly Glu Leu Gly Gln Pro Ser Gly Val Ala Ala Glu Arg  
35 40 45

Pro Cys Pro Thr Thr Cys Arg Cys Leu Gly Asp Leu Leu Asp Cys  
50 55 60

Ser Arg Lys Arg Leu Ala Arg Leu Pro Glu Pro Leu Pro Ser Trp  
65 70 75

Val Ala Arg Leu Asp Leu Ser His Asn Arg Leu Ser Phe Ile Lys  
80 85 90

Ala Ser Ser Met Ser His Leu Gln Ser Leu Arg Glu Val Lys Leu  
95 100 105

Asn Asn Asn Glu Leu Glu Thr Ile Pro Asn Leu Gly Pro Val Ser  
110 115 120

Ala Asn Ile Thr Leu Leu Ser Leu Ala Gly Asn Arg Ile Val Glu  
125 130 135

Ile Leu Pro Glu His Leu Lys Glu Phe Gln Ser Leu Glu Thr Leu  
140 145 150

Asp Leu Ser Ser Asn Asn Ile Ser Glu Leu Gln Thr Ala Phe Pro  
155 160 165

Ala Leu Gln Leu Lys Tyr Leu Tyr Leu Asn Ser Asn Arg Val Thr  
170 175 180

Ser Met Glu Pro Gly Tyr Phe Asp Asn Leu Ala Asn Thr Leu Leu  
185 190 195

Val Leu Lys Leu Asn Arg Asn Arg Ile Ser Ala Ile Pro Pro Lys  
200 205 210

Met Phe Lys Leu Pro Gln Leu Gln His Leu Glu Leu Asn Arg Asn

215	220	225
Lys Ile Lys Asn Val Asp Gly Leu Thr	Phe Gln Gly Leu Gly Ala	
230	235	240
Leu Lys Ser Leu Lys Met Gln Arg Asn	Gly Val Thr Lys Leu Met	
245	250	255
Asp Gly Ala Phe Trp Gly Leu Ser Asn	Met Glu Ile Leu Gln Leu	
260	265	270
Asp His Asn Asn Leu Thr Glu Ile Thr	Lys Gly Trp Leu Tyr Gly	
275	280	285
Leu Leu Met Leu Gln Glu Leu His Leu	Ser Gln Asn Ala Ile Asn	
290	295	300
Arg Ile Ser Pro Asp Ala Trp Glu Phe	Cys Gln Lys Leu Ser Glu	
305	310	315
Leu Asp Leu Thr Phe Asn His Leu Ser	Arg Leu Asp Asp Ser Ser	
320	325	330
Phe Leu Gly Leu Ser Leu Leu Asn Thr	Leu His Ile Gly Asn Asn	
335	340	345
Arg Val Ser Tyr Ile Ala Asp Cys Ala	Phe Arg Gly Leu Ser Ser	
350	355	360
Leu Lys Thr Leu Asp Leu Lys Asn Asn	Glu Ile Ser Trp Thr Ile	
365	370	375
Glu Asp Met Asn Gly Ala Phe Ser Gly	Leu Asp Lys Leu Arg Arg	
380	385	390
Leu Ile Leu Gln Gly Asn Arg Ile Arg	Ser Ile Thr Lys Lys Ala	
395	400	405
Phe Thr Gly Leu Asp Ala Leu Glu His	Leu Asp Leu Ser Asp Asn	
410	415	420
Ala Ile Met Ser Leu Gln Gly Asn Ala	Phe Ser Gln Met Lys Lys	
425	430	435
Leu Gln Gln Leu His Leu Asn Thr Ser	Ser Leu Leu Cys Asp Cys	
440	445	450
Gln Leu Lys Trp Leu Pro Gln Trp Val	Ala Glu Asn Asn Phe Gln	
455	460	465
Ser Phe Val Asn Ala Ser Cys Ala His	Pro Gln Leu Leu Lys Gly	
470	475	480

Arg Ser Ile Phe	Ala Val Ser Pro Asp Gly Phe Val Cys Asp Asp	485	490	495
Phe Pro Lys Pro	Gln Ile Thr Val Gln Pro Glu Thr Gln Ser Ala	500	505	510
Ile Lys Gly Ser	Asn Leu Ser Phe Ile Cys Ser Ala Ala Ser Ser	515	520	525
Ser Asp Ser Pro	Met Thr Phe Ala Trp Lys Lys Asp Asn Glu Leu	530	535	540
Leu His Asp Ala	Glu Met Glu Asn Tyr Ala His Leu Arg Ala Gln	545	550	555
Gly Gly Glu Val	Met Glu Tyr Thr Thr Ile Leu Arg Leu Arg Glu	560	565	570
Val Glu Phe Ala	Ser Glu Gly Lys Tyr Gln Cys Val Ile Ser Asn	575	580	585
His Phe Gly Ser	Ser Tyr Ser Val Lys Ala Lys Leu Thr Val Asn	590	595	600
Met Leu Pro Ser	Phe Thr Lys Thr Pro Met Asp Leu Thr Ile Arg	605	610	615
Ala Gly Ala Met	Ala Arg Leu Glu Cys Ala Ala Val Gly His Pro	620	625	630
Ala Pro Gln Ile	Ala Trp Gln Lys Asp Gly Gly Thr Asp Phe Pro	635	640	645
Ala Ala Arg Glu	Arg Arg Met His Val Met Pro Glu Asp Asp Val	650	655	660
Phe Phe Ile Val	Asp Val Lys Ile Glu Asp Ile Gly Val Tyr Ser	665	670	675
Cys Thr Ala Gln	Asn Ser Ala Gly Ser Ile Ser Ala Asn Ala Thr	680	685	690
Leu Thr Val Leu	Glu Thr Pro Ser Phe Leu Arg Pro Leu Leu Asp	695	700	705
Arg Thr Val Thr	Lys Gly Glu Thr Ala Val Leu Gln Cys Ile Ala	710	715	720
Gly Gly Ser Pro	Pro Pro Lys Leu Asn Trp Thr Lys Asp Asp Ser	725	730	735
Pro Leu Val Val	Thr Glu Arg His Phe Phe Ala Ala Gly Asn Gln	740	745	750

Leu	Leu	Ile	Ile	Val	Asp	Ser	Asp	Val	Ser	Asp	Ala	Gly	Lys	Tyr	
				755					760					765	
Thr	Cys	Glu	Met	Ser	Asn	Thr	Leu	Gly	Thr	Glu	Arg	Gly	Asn	Val	
				770					775					780	
Arg	Leu	Ser	Val	Ile	Pro	Thr	Pro	Thr	Cys	Asp	Ser	Pro	Gln	Met	
				785					790					795	
Thr	Ala	Pro	Ser	Leu	Asp	Asp	Asp	Gly	Trp	Ala	Thr	Val	Gly	Val	
				800					805					810	
Val	Ile	Ile	Ala	Val	Val	Cys	Cys	Val	Val	Gly	Thr	Ser	Leu	Val	
				815					820					825	
Trp	Val	Val	Ile	Ile	Tyr	His	Thr	Arg	Arg	Arg	Asn	Glu	Asp	Cys	
				830					835					840	
Ser	Ile	Thr	Asn	Thr	Asp	Glu	Thr	Asn	Leu	Pro	Ala	Asp	Ile	Pro	
				845					850					855	
Ser	Tyr	Leu	Ser	Ser	Gln	Gly	Thr	Leu	Ala	Asp	Arg	Gln	Asp	Gly	
				860					865					870	
Tyr	Val	Ser	Ser	Glu	Ser	Gly	Ser	His	His	Gln	Phe	Val	Thr	Ser	
				875					880					885	
Ser	Gly	Ala	Gly	Phe	Phe	Leu	Pro	Gln	His	Asp	Ser	Ser	Gly	Thr	
				890					895					900	
Cys	His	Ile	Asp	Asn	Ser	Ser	Glu	Ala	Asp	Val	Glu	Ala	Ala	Thr	
				905					910					915	
Asp	Leu	Phe	Leu	Cys	Pro	Phe	Leu	Gly	Ser	Thr	Gly	Pro	Met	Tyr	
				920					925					930	
Leu	Lys	Gly	Asn	Val	Tyr	Gly	Ser	Asp	Pro	Phe	Glu	Thr	Tyr	His	
				935					940					945	
Thr	Gly	Cys	Ser	Pro	Asp	Pro	Arg	Thr	Val	Leu	Met	Asp	His	Tyr	
				950					955					960	
Glu	Pro	Ser	Tyr	Ile	Lys	Lys	Lys	Glu	Cys	Tyr	Pro	Cys	Ser	His	
				965					970					975	
Pro	Ser	Glu	Glu	Ser	Cys	Glu	Arg	Ser	Phe	Ser	Asn	Ile	Ser	Trp	
				980					985					990	
Pro	Ser	His	Val	Arg	Lys	Leu	Leu	Asn	Thr	Ser	Tyr	Ser	His	Asn	
				995					1000					1005	
Glu	Gly	Pro	Gly	Met	Lys	Asn	Leu	Cys	Leu	Asn	Lys	Ser	Ser	Leu	

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Asp Phe Ser Ala Asn Pro Glu Pro Ala Ser Val Ala Ser Ser Asn		
1025	1030	1035
Ser Phe Met Gly Thr Phe Gly Lys Ala Leu Arg Arg Pro His Leu		
1040	1045	1050
Asp Ala Tyr Ser Ser Phe Gly Gln Pro Ser Asp Cys Gln Pro Arg		
1055	1060	1065
Ala Phe Tyr Leu Lys Ala His Ser Ser Pro Asp Leu Asp Ser Gly		
1070	1075	1080
Ser Glu Glu Asp Gly Lys Glu Arg Thr Asp Phe Gln Glu Glu Asn		
1085	1090	1095
His Ile Cys Thr Phe Lys Gln Thr Leu Glu Asn Tyr Arg Thr Pro		
1100	1105	1110
Asn Phe Gln Ser Tyr Asp Leu Asp Thr		
1115		

&lt;210&gt; 295

&lt;211&gt; 18

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 295

ggaaccgaat ctcagcta 18

&lt;210&gt; 296

&lt;211&gt; 19

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 296

cctaaactga actggacca 19

&lt;210&gt; 297

&lt;211&gt; 19

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe



<400> 297  
ggctggagac actgaacct 19

<210> 298  
<211> 24  
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<400> 298  
acagctgcac agctcagaac agtg 24

<210> 299

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<400> 299  
cattcccagt ataaaaattt tc 22

<210> 300  
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<210> 301  
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<400> 301  
gtgcctctcg gttaccacca atgg 24

<210> 302  
<211> 50  
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<220>

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<210> 303

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 303

gcctttgaca accttcagtc actagtgg 28

<210> 304

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 304

ccccatgtgt ccatgactgt tccc 24

<210> 305

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 305

tactgctca tgacctcttc actcccttgc atcatcttag agcgg 45

<210> 306

<211> 24

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<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 306

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<210> 307

<211> 24

<212> DNA  
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<220>  
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<400> 307  
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<210> 308  
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<400> 308  
 actccaagga aatcgatcc gttc 24

<210> 309  
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<220>  
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<400> 309  
 gccttcactg gtttggatgc attggagcat ctagacctga gtgacaacgc 50

<210> 310  
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 <212> DNA  
 <213> Homo Sapien

<400> 310  
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 cgagcccgcg gagcgcagct gagactgggg gagcgcgttc ggctgtggg 100  
 gcgcccgtcg gcgcggggc gcagcagga aggggaagct gtggtctgcc 150  
 ctgctccacg aggcgccact ggtgtgaacc gggagagccc ctgggtggtc 200  
 ccgtccccta tccctccttt atatagaaac cttccacact ggggaaggcag 250  
 cggcgaggca ggagggtca tggtagcaa ggaggccggc tgatctgcag 300  
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 gaggaggcag aacagcctgc ctggttccat cagccctggc gccagggcg 400

atctgactcg gcacccctg caggcaccat ggcccagagc cgggtgctgc 450  
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<220>  
 <223> Synthetic Oligonucleotide Probe

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<210> 312  
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<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 312  
 gcggccacgg tccttgga aa tg 22

<210> 313  
 <211> 45  
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<400> 313  
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<210> 314  
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 <212> DNA  
 <213> Homo Sapien

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gggttcctcg agactctcag aggggcgcct cccatcggcg cccaccaccc 150  
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 catcttggtt attatttaat gttttctaaa ataaaaaatg ttagtggttt 2950  
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 aat 3003

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<211> 509

<212> PRT

<213> Homo Sapien

<400> 315

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Ser	Ser	Ile	Gly	Leu	Cys	Arg	Tyr	Gly	Gly	Arg	Ile	Asp	Cys	Cys	35	40	45	
Trp	Gly	Trp	Ala	Arg	Gln	Ser	Trp	Gly	Gln	Cys	Gln	Pro	Val	Cys	50	55	60	
Gln	Pro	Arg	Cys	Lys	His	Gly	Glu	Cys	Ile	Gly	Pro	Asn	Lys	Cys	65	70	75	
Lys	Cys	His	Pro	Gly	Tyr	Ala	Gly	Lys	Thr	Cys	Asn	Gln	Asp	Leu	80	85	90	
Asn	Glu	Cys	Gly	Leu	Lys	Pro	Arg	Pro	Cys	Lys	His	Arg	Cys	Met	95	100	105	
Asn	Thr	Tyr	Gly	Ser	Tyr	Lys	Cys	Tyr	Cys	Leu	Asn	Gly	Tyr	Met	110	115	120	
Leu	Met	Pro	Asp	Gly	Ser	Cys	Ser	Ser	Ala	Leu	Thr	Cys	Ser	Met	125	130	135	
Ala	Asn	Cys	Gln	Tyr	Gly	Cys	Asp	Val	Val	Lys	Gly	Gln	Ile	Arg	140	145	150	
Cys	Gln	Cys	Pro	Ser	Pro	Gly	Leu	His	Leu	Ala	Pro	Asp	Gly	Arg	155	160	165	

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Pro Arg Phe Arg	Gln Cys Val Asn Thr	Phe Gly Ser Tyr Ile Cys
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Lys Cys His Lys	Gly Phe Asp Leu Met	Tyr Ile Gly Gly Lys Tyr
200		205 210
Gln Cys His Asp	Ile Asp Glu Cys Ser	Leu Gly Gln Tyr Gln Cys
215		220 225
Ser Ser Phe Ala	Arg Cys Tyr Asn Val	Arg Gly Ser Tyr Lys Cys
230		235 240
Lys Cys Lys Glu	Gly Tyr Gln Gly Asp	Gly Leu Thr Cys Val Tyr
245		250 255
Ile Pro Lys Val	Met Ile Glu Pro Ser	Gly Pro Ile His Val Pro
260		265 270
Lys Gly Asn Gly	Thr Ile Leu Lys Gly	Asp Thr Gly Asn Asn Asn
275		280 285
Trp Ile Pro Asp	Val Gly Ser Thr Trp	Trp Pro Pro Lys Thr Pro
290		295 300
Tyr Ile Pro Pro	Ile Ile Thr Asn Arg	Pro Thr Ser Lys Pro Thr
305		310 315
Thr Arg Pro Thr	Pro Lys Pro Thr Pro	Ile Pro Thr Pro Pro Pro
320		325 330
Pro Pro Pro Leu	Pro Thr Glu Leu Arg	Thr Pro Leu Pro Pro Thr
335		340 345
Thr Pro Glu Arg	Pro Thr Thr Gly Leu	Thr Thr Ile Ala Pro Ala
350		355 360
Ala Ser Thr Pro	Pro Gly Gly Ile Thr	Val Asp Asn Arg Val Gln
365		370 375
Thr Asp Pro Gln	Lys Pro Arg Gly Asp	Val Phe Ser Val Leu Val
380		385 390
His Ser Cys Asn	Phe Asp His Gly Leu	Cys Gly Trp Ile Arg Glu
395		400 405
Lys Asp Asn Asp	Leu His Trp Glu Pro	Ile Arg Asp Pro Ala Gly
410		415 420
Gly Gln Tyr Leu	Thr Val Ser Ala Ala	Lys Ala Pro Gly Gly Lys

425	430	435
Ala Ala Arg Leu Val Leu Pro Leu Gly	Arg Leu Met His Ser Gly	
440	445	450
Asp Leu Cys Leu Ser Phe Arg His Lys	Val Thr Gly Leu His Ser	
455	460	465
Gly Thr Leu Gln Val Phe Val Arg Lys	His Gly Ala His Gly Ala	
470	475	480
Ala Leu Trp Gly Arg Asn Gly Gly His	Gly Trp Arg Gln Thr Gln	
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Ile Thr Leu Arg Gly Ala Asp Ile Lys	Ser Glu Ser Gln Arg	
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<210> 316  
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<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 316  
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<210> 317  
 <211> 24  
 <212> DNA  
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<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 317  
 ttgcacttgt aggacccacg tacg 24

<210> 318  
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<210> 319  
 <211> 2110  
 <212> DNA

<213> Homo Sapien

<400> 319

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 aaaaaaaaaa 2110

<210> 320

<211> 450

<212> PRT

<213> Homo Sapien

<400> 320

Met	Trp	Leu	Lys	Val	Phe	Thr	Thr	Phe	Leu	Ser	Phe	Ala	Thr	Gly
1				5					10					15

Ala	Cys	Ser	Gly	Leu	Lys	Val	Thr	Val	Pro	Ser	His	Thr	Val	His
				20					25					30

Gly	Val	Arg	Gly	Gln	Ala	Leu	Tyr	Leu	Pro	Val	His	Tyr	Gly	Phe
				35					40					45

His	Thr	Pro	Ala	Ser	Asp	Ile	Gln	Ile	Ile	Trp	Leu	Phe	Glu	Arg
				50					55					60

Pro His Thr Met	Pro Lys Tyr Leu Leu Gly Ser Val Asn Lys Ser	65	70	75
Val Val Pro Asp	Leu Glu Tyr Gln His Lys Phe Thr Met Met Pro	80	85	90
Pro Asn Ala Ser	Leu Leu Ile Asn Pro Leu Gln Phe Pro Asp Glu	95	100	105
Gly Asn Tyr Ile	Val Lys Val Asn Ile Gln Gly Asn Gly Thr Leu	110	115	120
Ser Ala Ser Gln	Lys Ile Gln Val Thr Val Asp Asp Pro Val Thr	125	130	135
Lys Pro Val Val	Gln Ile His Pro Pro Ser Gly Ala Val Glu Tyr	140	145	150
Val Gly Asn Met	Thr Leu Thr Cys His Val Glu Gly Gly Thr Arg	155	160	165
Leu Ala Tyr Gln	Trp Leu Lys Asn Gly Arg Pro Val His Thr Ser	170	175	180
Ser Thr Tyr Ser	Phe Ser Pro Gln Asn Asn Thr Leu His Ile Ala	185	190	195
Pro Val Thr Lys	Glu Asp Ile Gly Asn Tyr Ser Cys Leu Val Arg	200	205	210
Asn Pro Val Ser	Glu Met Glu Ser Asp Ile Ile Met Pro Ile Ile	215	220	225
Tyr Tyr Gly Pro	Tyr Gly Leu Gln Val Asn Ser Asp Lys Gly Leu	230	235	240
Lys Val Gly Glu	Val Phe Thr Val Asp Leu Gly Glu Ala Ile Leu	245	250	255
Phe Asp Cys Ser	Ala Asp Ser His Pro Pro Asn Thr Tyr Ser Trp	260	265	270
Ile Arg Arg Thr	Asp Asn Thr Thr Tyr Ile Ile Lys His Gly Pro	275	280	285
Arg Leu Glu Val	Ala Ser Glu Lys Val Ala Gln Lys Thr Met Asp	290	295	300
Tyr Val Cys Cys	Ala Tyr Asn Asn Ile Thr Gly Arg Gln Asp Glu	305	310	315
Thr His Phe Thr	Val Ile Ile Thr Ser Val Gly Leu Glu Lys Leu			

320	325	330
Ala Gln Lys Gly Lys Ser Leu Ser Pro Leu Ala Ser Ile Thr Gly		
335	340	345
Ile Ser Leu Phe Leu Ile Ile Ser Met Cys Leu Leu Phe Leu Trp		
350	355	360
Lys Lys Tyr Gln Pro Tyr Lys Val Ile Lys Gln Lys Leu Glu Gly		
365	370	375
Arg Pro Glu Thr Glu Tyr Arg Lys Ala Gln Thr Phe Ser Gly His		
380	385	390
Glu Asp Ala Leu Asp Asp Phe Gly Ile Tyr Glu Phe Val Ala Phe		
395	400	405
Pro Asp Val Ser Gly Val Ser Arg Ile Pro Ser Arg Ser Val Pro		
410	415	420
Ala Ser Asp Cys Val Ser Gly Gln Asp Leu His Ser Thr Val Tyr		
425	430	435
Glu Val Ile Gln His Ile Pro Ala Gln Gln Gln Asp His Pro Glu		
440	445	450

&lt;210&gt; 321

&lt;211&gt; 25

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 321

gatacctgtca caaagccagt ggtgc 25

&lt;210&gt; 322

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 322

cactgacagg gttcctcacc cagg 24

&lt;210&gt; 323

&lt;211&gt; 45

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 323

ctccctctgg gctgtggagt atgtggggaa catgaccctg acatg 45

&lt;210&gt; 324

&lt;211&gt; 2397

&lt;212&gt; DNA

&lt;213&gt; Homo Sapien

&lt;400&gt; 324

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cctgggtgctg ttgctttggg gtgctccctg gacgcacggg cggcggagca 100  
acgttcgcgt catcacggac gagaactgga gagaactgct ggaaggagac 150  
tggatgatag aattttatgc cccgtgggtgc cctgcttgct aaaatcttca 200  
accggaatgg gaaagttttg ctgaatgggg agaagatctt gaggttaata 250  
ttgcgaaagt agatgtcaca gagcagccag gactgagtgg acggtttata 300  
ataactgctc ttctactat ttatcattgt aaagatgggtg aatttaggcg 350  
ctatcagggg ccaaggacta agaaggactt cataaacttt ataagtata 400  
aagagtggaa gagtattgag cccgtttcat catggtttgg tccaggttct 450  
gttctgatga gtagtatgtc agcactcttt cagctatcta tgtggatcag 500  
gacgtgccat aactacttta ttgaagacct tggattgcca gtgtggggat 550  
catatactgt ttttgcttta gcaactctgt tttccggact gttattagga 600  
ctctgtatga tatttgtggc agattgcctt tgtccttcaa aaaggcgcag 650  
accacagcca taccataacc cttcaaaaaa attattatca gaatctgcac 700  
aacctttgaa aaaagtggag gaggaacaag aggcggatga agaagatggt 750  
tcagaagaag aagctgaaag taaagaagga acaaacaag actttccaca 800  
gaatgccata agacaacgct ctctgggtcc atcattggcc acagataaat 850  
cctagttaaa ttttatagtt atcttaatat tatgattttg ataaaaacag 900  
aagattgac attttgtttg gtttgaagtg aactgtgact ttttgaata 950  
ttgcaggggt cagtctagat tgtcattaaa ttgaagagtc tacattcaga 1000



acataaaaagc actaggtata caagtttgaa atatgattta agcacagtat 1050  
gatgggtttaa atagttctct aatttttgaa aaatcgtgcc aagcaataag 1100  
atztatgtat atttgtttaa taataaccta tttcaagtct gagttttgaa 1150  
aatttacatt tcccaagtat tgcattattg aggtatttaa gaagattatt 1200  
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caaaatttcc ttgtattttt aggttatgca actaataaaa actaccttac 1400  
attaattaat tacagtttcc tacacatggg aatacaggat atgctactga 1450  
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attttctctt gtatttttct tacttactat gggttacatt ttttattttt 1550  
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tatttttttg ttgtttcaaa ctgaagttta ctgagagatc catcaaattg 1650  
aacaatctgt tgtaatttaa aattttggcc acttttttca gattttacat 1700  
cattcttget gaacttcaac ttgaaattgt ttttttttcc tttttggatg 1750  
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ttctttaaag ccctctcctt tagaatttaa aatattgtac cattaaagag 2300  
tttgatgtg taacttgtga tgcccttagaa aaatatecta agcacaaaat 2350

aaacctttct aaccacttca ttaaagctga aaaaaaaaaa aaaaaaa 2397

<210> 325

<211> 280

<212> PRT

<213> Homo Sapien

<400> 325

Met	Ala	Pro	Ser	Gly	Ser	Leu	Ala	Val	Pro	Leu	Ala	Val	Leu	Val	15
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Leu	Leu	Leu	Trp	Gly	Ala	Pro	Trp	Thr	His	Gly	Arg	Arg	Ser	Asn	30
				20					25						
Val	Arg	Val	Ile	Thr	Asp	Glu	Asn	Trp	Arg	Glu	Leu	Leu	Glu	Gly	45
				35					40						
Asp	Trp	Met	Ile	Glu	Phe	Tyr	Ala	Pro	Trp	Cys	Pro	Ala	Cys	Gln	60
				50					55						
Asn	Leu	Gln	Pro	Glu	Trp	Glu	Ser	Phe	Ala	Glu	Trp	Gly	Glu	Asp	75
				65					70						
Leu	Glu	Val	Asn	Ile	Ala	Lys	Val	Asp	Val	Thr	Glu	Gln	Pro	Gly	90
				80					85						
Leu	Ser	Gly	Arg	Phe	Ile	Ile	Thr	Ala	Leu	Pro	Thr	Ile	Tyr	His	105
				95					100						
Cys	Lys	Asp	Gly	Glu	Phe	Arg	Arg	Tyr	Gln	Gly	Pro	Arg	Thr	Lys	120
				110					115						
Lys	Asp	Phe	Ile	Asn	Phe	Ile	Ser	Asp	Lys	Glu	Trp	Lys	Ser	Ile	135
				125					130						
Glu	Pro	Val	Ser	Ser	Trp	Phe	Gly	Pro	Gly	Ser	Val	Leu	Met	Ser	150
				140					145						
Ser	Met	Ser	Ala	Leu	Phe	Gln	Leu	Ser	Met	Trp	Ile	Arg	Thr	Cys	165
				155					160						
His	Asn	Tyr	Phe	Ile	Glu	Asp	Leu	Gly	Leu	Pro	Val	Trp	Gly	Ser	180
				170					175						
Tyr	Thr	Val	Phe	Ala	Leu	Ala	Thr	Leu	Phe	Ser	Gly	Leu	Leu	Leu	195
				185					190						
Gly	Leu	Cys	Met	Ile	Phe	Val	Ala	Asp	Cys	Leu	Cys	Pro	Ser	Lys	210
				200					205						
Arg	Arg	Arg	Pro	Gln	Pro	Tyr	Pro	Tyr	Pro	Ser	Lys	Lys	Leu	Leu	

215	220	225
Ser Glu Ser Ala Gln Pro Leu Lys Lys Val Glu Glu Glu Gln Glu		
230	235	240
Ala Asp Glu Glu Asp Val Ser Glu Glu Glu Ala Glu Ser Lys Glu		
245	250	255
Gly Thr Asn Lys Asp Phe Pro Gln Asn Ala Ile Arg Gln Arg Ser		
260	265	270
Leu Gly Pro Ser Leu Ala Thr Asp Lys Ser		
275	280	

&lt;210&gt; 326

&lt;211&gt; 23

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 326

tgaggtgggc aagcggcgaa atg 23

&lt;210&gt; 327

&lt;211&gt; 20

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 327

tatgtggatc aggacgtgcc 20

&lt;210&gt; 328

&lt;211&gt; 21

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 328

tgcaggggttc agtctagatt g 21

&lt;210&gt; 329

&lt;211&gt; 25

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 329

ttgaaggaca aaggcaatct gccac 25

<210> 330

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 330

ggagtcttgc agttcccctg gcagtcctgg tgctgttgct ttggg 45

<210> 331

<211> 2168

<212> DNA

<213> Homo Sapien

<400> 331

gcgagtgtcc agctgcggag acccgtgata attcgtaac taattcaaca 50  
 aacgggaccc ttctgtgtgc cagaaaccgc aagcagttgc taaccagtg 100  
 ggacaggcgg attggaagag cgggaaggtc ctggcccaga gcagtgtgac 150  
 acttcctct gtgaccatga aactctgggt gtctgcattg ctgatggcct 200  
 ggtttgggtgt cctgagctgt gtgcaggccg aattcttcac ctctattggg 250  
 cacatgactg acctgattta tgcagagaaa gagctggtgc agtctctgaa 300  
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 ccaacaaaat ggaagccttg actagcaagt cagctgctga tgctgagggc 400  
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gcttgatgcc ggggaggagg ccaccacaac caagtcacag gtgctggact 800  
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 ctgcagaatt gttacagggt gcaaattatg gagtgggagg acagtatgaa 1450  
 ccgcacttcg acttctctag gcgacctttt gacagcggcc tcaaacaga 1500  
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 ggtacagctg tgttctggta caacctcttg cggagcgggg aagggtgacta 1650  
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 gttagctgtc tagcgcttag caaggctcct ttgtacctca ggtgttttag 2050  
 gtgtgagatg tttcagtga ccaaagttct gataccttgt ttacatgttt 2100

gtttttatgg catttctatc tattgtggct ttaccaaaaa ataaaatgtc 2150

cctaccagaa aaaaaaaaa 2168

<210> 332

<211> 533

<212> PRT

<213> Homo Sapien

<400> 332

Met Lys Leu Trp Val Ser Ala Leu Leu Met Ala Trp Phe Gly Val  
1 5 10 15

Leu Ser Cys Val Gln Ala Glu Phe Phe Thr Ser Ile Gly His Met  
20 25 30

Thr Asp Leu Ile Tyr Ala Glu Lys Glu Leu Val Gln Ser Leu Lys  
35 40 45

Glu Tyr Ile Leu Val Glu Glu Ala Lys Leu Ser Lys Ile Lys Ser  
50 55 60

Trp Ala Asn Lys Met Glu Ala Leu Thr Ser Lys Ser Ala Ala Asp  
65 70 75

Ala Glu Gly Tyr Leu Ala His Pro Val Asn Ala Tyr Lys Leu Val  
80 85 90

Lys Arg Leu Asn Thr Asp Trp Pro Ala Leu Glu Asp Leu Val Leu  
95 100 105

Gln Asp Ser Ala Ala Gly Phe Ile Ala Asn Leu Ser Val Gln Arg  
110 115 120

Gln Phe Phe Pro Thr Asp Glu Asp Glu Ile Gly Ala Ala Lys Ala  
125 130 135

Leu Met Arg Leu Gln Asp Thr Tyr Arg Leu Asp Pro Gly Thr Ile  
140 145 150

Ser Arg Gly Glu Leu Pro Gly Thr Lys Tyr Gln Ala Met Leu Ser  
155 160 165

Val Asp Asp Cys Phe Gly Met Gly Arg Ser Ala Tyr Asn Glu Gly  
170 175 180

Asp Tyr Tyr His Thr Val Leu Trp Met Glu Gln Val Leu Lys Gln  
185 190 195

Leu Asp Ala Gly Glu Glu Ala Thr Thr Thr Lys Ser Gln Val Leu  
200 205 210

Asp Tyr Leu Ser	Tyr Ala Val Phe Gln Leu Gly Asp Leu His Arg	215	220	225
Ala Leu Glu Leu Thr Arg Arg Leu Leu Ser Leu Asp Pro Ser His		230	235	240
Glu Arg Ala Gly Gly Asn Leu Arg Tyr Phe Glu Gln Leu Leu Glu		245	250	255
Glu Glu Arg Glu Lys Thr Leu Thr Asn Gln Thr Glu Ala Glu Leu		260	265	270
Ala Thr Pro Glu Gly Ile Tyr Glu Arg Pro Val Asp Tyr Leu Pro		275	280	285
Glu Arg Asp Val Tyr Glu Ser Leu Cys Arg Gly Glu Gly Val Lys		290	295	300
Leu Thr Pro Arg Arg Gln Lys Arg Leu Phe Cys Arg Tyr His His		305	310	315
Gly Asn Arg Ala Pro Gln Leu Leu Ile Ala Pro Phe Lys Glu Glu		320	325	330
Asp Glu Trp Asp Ser Pro His Ile Val Arg Tyr Tyr Asp Val Met		335	340	345
Ser Asp Glu Glu Ile Glu Arg Ile Lys Glu Ile Ala Lys Pro Lys		350	355	360
Leu Ala Arg Ala Thr Val Arg Asp Pro Lys Thr Gly Val Leu Thr		365	370	375
Val Ala Ser Tyr Arg Val Ser Lys Ser Ser Trp Leu Glu Glu Asp		380	385	390
Asp Asp Pro Val Val Ala Arg Val Asn Arg Arg Met Gln His Ile		395	400	405
Thr Gly Leu Thr Val Lys Thr Ala Glu Leu Leu Gln Val Ala Asn		410	415	420
Tyr Gly Val Gly Gly Gln Tyr Glu Pro His Phe Asp Phe Ser Arg		425	430	435
Arg Pro Phe Asp Ser Gly Leu Lys Thr Glu Gly Asn Arg Leu Ala		440	445	450
Thr Phe Leu Asn Tyr Met Ser Asp Val Glu Ala Gly Gly Ala Thr		455	460	465
Val Phe Pro Asp Leu Gly Ala Ala Ile Trp Pro Lys Lys Gly Thr		470	475	480

Ala Val Phe Trp Tyr Asn Leu Leu Arg Ser Gly Glu Gly Asp Tyr  
                           485                          490                          495

Arg Thr Arg His Ala Ala Cys Pro Val Leu Val Gly Cys Lys Trp  
                           500                          505                          510

Val Ser Asn Lys Trp Phe His Glu Arg Gly Gln Glu Phe Leu Arg  
                           515                          520                          525

Pro Cys Gly Ser Thr Glu Val Asp  
                           530

<210> 333

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 333

ccaggcacaa tttccaga 18

<210> 334

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 334

ggacccttct gtgtgccag 19

<210> 335

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 335

ggtctcaaga actcctgtc 19

<210> 336

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe



<400> 336  
acactcagca ttgcctggta cttg 24

<210> 337  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 337  
gggcacatga ctgacctgat ttatgcagag aaagagctgg tgcag 45

<210> 338  
<211> 2789

<212> DNA  
<213> Homo Sapien

<400> 338  
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<210> 339

<211> 772

<212> PRT

<213> Homo Sapien

<400> 339

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			20						25					30

Val	Ser	Trp	Ile	Gln	Gly	Glu	Gly	Glu	Asp	Pro	Cys	Val	Glu	Ala
			35						40					45

Val	Gly	Glu	Arg	Gly	Gly	Pro	Gln	Asn	Pro	Asp	Ser	Arg	Ala	Arg
			50						55					60

Leu	Asp	Gln	Ser	Asp	Glu	Asp	Phe	Lys	Pro	Arg	Ile	Val	Pro	Tyr
			65						70					75

Tyr	Arg	Asp	Pro	Asn	Lys	Pro	Tyr	Lys	Lys	Val	Leu	Arg	Thr	Arg
			80						85					90

Tyr	Ile	Gln	Thr	Glu	Leu	Gly	Ser	Arg	Glu	Arg	Leu	Leu	Val	Ala
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

	95		100		105
Val Leu Thr Ser	Arg Ala Thr Leu Ser	Thr Leu Ala Val Ala Val			
	110		115		120
Asn Arg Thr Val	Ala His His Phe Pro	Arg Leu Leu Tyr Phe Thr			
	125		130		135
Gly Gln Arg Gly	Ala Arg Ala Pro Ala	Gly Met Gln Val Val Ser			
	140		145		150
His Gly Asp Glu	Arg Pro Ala Trp Leu	Met Ser Glu Thr Leu Arg			
	155		160		165
His Leu His Thr	His Phe Gly Ala Asp	Tyr Asp Trp Phe Phe Ile			
	170		175		180
Met Gln Asp Asp	Thr Tyr Val Gln Ala	Pro Arg Leu Ala Ala Leu			
	185		190		195
Ala Gly His Leu	Ser Ile Asn Gln Asp	Leu Tyr Leu Gly Arg Ala			
	200		205		210
Glu Glu Phe Ile	Gly Ala Gly Glu Gln	Ala Arg Tyr Cys His Gly			
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Gly Phe Gly Tyr	Leu Leu Ser Arg Ser	Leu Leu Leu Arg Leu Arg			
	230		235		240
Pro His Leu Asp	Gly Cys Arg Gly Asp	Ile Leu Ser Ala Arg Pro			
	245		250		255
Asp Glu Trp Leu	Gly Arg Cys Leu Ile	Asp Ser Leu Gly Val Gly			
	260		265		270
Cys Val Ser Gln	His Gln Gly Gln Gln	Tyr Arg Ser Phe Glu Leu			
	275		280		285
Ala Lys Asn Arg	Asp Pro Glu Lys Glu	Gly Ser Ser Ala Phe Leu			
	290		295		300
Ser Ala Phe Ala	Val His Pro Val Ser	Glu Gly Thr Leu Met Tyr			
	305		310		315
Arg Leu His Lys	Arg Phe Ser Ala Leu	Glu Leu Glu Arg Ala Tyr			
	320		325		330
Ser Glu Ile Glu	Gln Leu Gln Ala Gln	Ile Arg Asn Leu Thr Val			
	335		340		345
Leu Thr Pro Glu	Gly Glu Ala Gly Leu	Ser Trp Pro Val Gly Leu			
	350		355		360

Pro Ala Pro Phe Thr Pro His Ser Arg Phe Glu Val Leu Gly Trp	365	370	375
Asp Tyr Phe Thr Glu Gln His Thr Phe Ser Cys Ala Asp Gly Ala	380	385	390
Pro Lys Cys Pro Leu Gln Gly Ala Ser Arg Ala Asp Val Gly Asp	395	400	405
Ala Leu Glu Thr Ala Leu Glu Gln Leu Asn Arg Arg Tyr Gln Pro	410	415	420
Arg Leu Arg Phe Gln Lys Gln Arg Leu Leu Asn Gly Tyr Arg Arg	425	430	435
Phe Asp Pro Ala Arg Gly Met Glu Tyr Thr Leu Asp Leu Leu Leu	440	445	450
Glu Cys Val Thr Gln Arg Gly His Arg Arg Ala Leu Ala Arg Arg	455	460	465
Val Ser Leu Leu Arg Pro Leu Ser Arg Val Glu Ile Leu Pro Met	470	475	480
Pro Tyr Val Thr Glu Ala Thr Arg Val Gln Leu Val Leu Pro Leu	485	490	495
Leu Val Ala Glu Ala Ala Ala Ala Pro Ala Phe Leu Glu Ala Phe	500	505	510
Ala Ala Asn Val Leu Glu Pro Arg Glu His Ala Leu Leu Thr Leu	515	520	525
Leu Leu Val Tyr Gly Pro Arg Glu Gly Gly Arg Gly Ala Pro Asp	530	535	540
Pro Phe Leu Gly Val Lys Ala Ala Ala Ala Glu Leu Glu Arg Arg	545	550	555
Tyr Pro Gly Thr Arg Leu Ala Trp Leu Ala Val Arg Ala Glu Ala	560	565	570
Pro Ser Gln Val Arg Leu Met Asp Val Val Ser Lys Lys His Pro	575	580	585
Val Asp Thr Leu Phe Phe Leu Thr Thr Val Trp Thr Arg Pro Gly	590	595	600
Pro Glu Val Leu Asn Arg Cys Arg Met Asn Ala Ile Ser Gly Trp	605	610	615
Gln Ala Phe Phe Pro Val His Phe Gln Glu Phe Asn Pro Ala Leu	620	625	630

Ser Pro Gln Arg Ser Pro Pro Gly Pro Pro Gly Ala Gly Pro Asp  
 635 640 645  
 Pro Pro Ser Pro Pro Gly Ala Asp Pro Ser Arg Gly Ala Pro Ile  
 650 655 660  
 Gly Gly Arg Phe Asp Arg Gln Ala Ser Ala Glu Gly Cys Phe Tyr  
 665 670 675  
 Asn Ala Asp Tyr Leu Ala Ala Arg Ala Arg Leu Ala Gly Glu Leu  
 680 685 690  
 Ala Gly Gln Glu Glu Glu Glu Ala Leu Glu Gly Leu Glu Val Met  
 695 700 705  
 Asp Val Phe Leu Arg Phe Ser Gly Leu His Leu Phe Arg Ala Val  
 710 715 720  
 Glu Pro Gly Leu Val Gln Lys Phe Ser Leu Arg Asp Cys Ser Pro  
 725 730 735  
 Arg Leu Ser Glu Glu Leu Tyr His Arg Cys Arg Leu Ser Asn Leu  
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 Glu Gly Leu Gly Gly Arg Ala Gln Leu Ala Met Ala Leu Phe Glu  
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 tgctaggaca cattaggatt ggtcatggaa atagaatgca ccaccatgag 200  
 catcatcacc tacaagctcc taacaaagaa gatatcttga aaatttcaga 250  
 ggatgagcgc atggagctca gtaagagctt tcgagtatac tgtattatcc 300  
 ttgtaaaacc caaagatgtg agtccttggg ctgcagtaaa ggagacttgg 350  
 accaaacact gtgacaaaagc agagttcttc agttctgaaa atgttaaagt 400

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 aagcttaciaa atacgccttt gataagtata gagaccaata caactgggtc 500  
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 tttgttaaaa aaggatccat cacagccttt ctatctaggc cacactataa 600  
 aatctggaga ccttgaatat gtgggtatgg aaggaggaat tgtcttaagt 650  
 gtagaatcaa tgaaaagact taacagcctt ctcaatatcc cagaaaagt 700  
 tcctgaacag ggagggatga tttggaagat atctgaagat aaacagctag 750  
 cagtttgctt gaaatatgct ggagtatttg cagaaaatgc agaagatgct 800  
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<211> 318

<212> PRT

<213> Homo Sapien

&lt;400&gt; 341

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Gly	His	Gly	Asn	Arg	Met	His	His	His	Glu	His	His	His	Leu	Gln	35	40	45	
Ala	Pro	Asn	Lys	Glu	Asp	Ile	Leu	Lys	Ile	Ser	Glu	Asp	Glu	Arg	50	55	60	
Met	Glu	Leu	Ser	Lys	Ser	Phe	Arg	Val	Tyr	Cys	Ile	Ile	Leu	Val	65	70	75	
Lys	Pro	Lys	Asp	Val	Ser	Leu	Trp	Ala	Ala	Val	Lys	Glu	Thr	Trp	80	85	90	
Thr	Lys	His	Cys	Asp	Lys	Ala	Glu	Phe	Phe	Ser	Ser	Glu	Asn	Val	95	100	105	
Lys	Val	Phe	Glu	Ser	Ile	Asn	Met	Asp	Thr	Asn	Asp	Met	Trp	Leu	110	115	120	
Met	Met	Arg	Lys	Ala	Tyr	Lys	Tyr	Ala	Phe	Asp	Lys	Tyr	Arg	Asp	125	130	135	
Gln	Tyr	Asn	Trp	Phe	Phe	Leu	Ala	Arg	Pro	Thr	Thr	Phe	Ala	Ile	140	145	150	
Ile	Glu	Asn	Leu	Lys	Tyr	Phe	Leu	Leu	Lys	Lys	Asp	Pro	Ser	Gln	155	160	165	
Pro	Phe	Tyr	Leu	Gly	His	Thr	Ile	Lys	Ser	Gly	Asp	Leu	Glu	Tyr	170	175	180	
Val	Gly	Met	Glu	Gly	Gly	Ile	Val	Leu	Ser	Val	Glu	Ser	Met	Lys	185	190	195	
Arg	Leu	Asn	Ser	Leu	Leu	Asn	Ile	Pro	Glu	Lys	Cys	Pro	Glu	Gln	200	205	210	
Gly	Gly	Met	Ile	Trp	Lys	Ile	Ser	Glu	Asp	Lys	Gln	Leu	Ala	Val	215	220	225	
Cys	Leu	Lys	Tyr	Ala	Gly	Val	Phe	Ala	Glu	Asn	Ala	Glu	Asp	Ala	230	235	240	
Asp	Gly	Lys	Asp	Val	Phe	Asn	Thr	Lys	Ser	Val	Gly	Leu	Ser	Ile	245	250	255	
Lys	Glu	Ala	Met	Thr	Tyr	His	Pro	Asn	Gln	Val	Val	Glu	Gly	Cys				



	260		265		270
Cys Ser Asp Met	Ala Val Thr Phe Asn Gly	Leu Thr Pro Asn Gln			
	275		280		285
Met His Val Met	Met Tyr Gly Val Tyr Arg	Leu Arg Ala Phe Gly			
	290		295		300
His Ile Phe Asn	Asp Ala Leu Val Phe	Leu Pro Pro Asn Gly	Ser		
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Asp Asn Asp

<210> 342

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 342

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<210> 343

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 343

ctggttcttc cttgcacg 18

<210> 344

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 344

gcccaaagtc cctaaggcgg tatacccc 28

<210> 345

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 345

gggtgtgatg cttggaagca ttttctgtgc ttgatcact atgctaggac 50

<210> 346

<211> 25

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<213> Artificial Sequence

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<400> 346

gggatgcagg tgggtgtctca tgggg 25

<210> 347

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 347

ccctcatgta ccggctcc 18

<210> 348

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 348

ggatttcta atcagactcact atagggctca gaaaagcgca acagagaa 48

<210> 349

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 349

ctatgaaatt aaccctcact aaagggatgt cttccatgcc aaccttc 47

<210> 350

<211> 48

<212> DNA

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<220>  
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<400> 350  
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<210> 351  
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<220>  
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<400> 351  
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<210> 352  
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<400> 352  
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<210> 353  
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<220>  
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<400> 353  
ctatgaaattaacctcactaaagggacggggacaccacggaccaga 48

<210> 354  
<211> 48  
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<220>  
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<400> 354  
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<210> 355  
<211> 48

<212> DNA  
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<400> 355  
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<210> 356  
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<212> DNA  
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<400> 356  
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<210> 357  
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<212> DNA  
<213> Artificial Sequence

<220>  
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<210> 358  
<211> 47  
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<213> Artificial Sequence

<220>  
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<400> 358  
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<210> 359  
<211> 48  
<212> DNA  
<213> Artificial Sequence

<220>  
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<400> 359  
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<210> 360  
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<220>  
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<400> 360  
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<210> 361  
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<212> DNA  
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<400> 361  
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<210> 362  
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<220>  
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<400> 362  
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<210> 363  
<211> 48  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 363  
ctatgaaatt aaccctcact aaagggagga ttgccgcgac cctcacag 48

<210> 364  
<211> 47  
<212> DNA  
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<220>  
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<400> 364

ggattctaatac gactcact atagggcccc tctgccttc cctgtcc 47

<210> 365

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

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<400> 365

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<210> 366

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 366

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<210> 367

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 367

ctatgaaatt aaccctcact aaaggacag acggggcaga gggagtg 47

<210> 368

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 368

ggattctaatac gactcact atagggccag gaggcgtgag gagaaac 47

<210> 369

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 369

ctatgaaatt aaccctcact aaagggaaag acatgtcatc gggagtgg 48

<210> 370

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 370

ggattctaatac gactcact atagggccgg gtggaggtgg aacagaaa 48

<210> 371

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 371

ctatgaaatt aaccctcact aaaggacac agacagagcc ccatacgc 48

<210> 372

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 372

ggattctaatac gactcact atagggccag ggaaatccgg atgtctc 47

<210> 373

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 373

ctatgaaatt aaccctcact aaaggagta aggggatgcc accgagta 48

<210> 374

<211> 47

<212> DNA

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<400> 374  
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<210> 375  
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<400> 375  
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<210> 376  
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 <213> Homo Sapien

<400> 376  
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 aaaaaatgaa ttcattctaaa tcattctgaaa cacaatgcac agagagagga 150  
 tgctttctctt cccaaatgtt cttatggact gttgctggga tccccatcct 200  
 atttctcagt gcctgtttca tcaccagatg tggtgtgaca tttegcattct 250  
 ttcaaacctg tgatgagaaa aagtttcagc tacctgagaa tttcacagag 300  
 ctctctgtgt acaattatgg atcaggttca gtcaagaatt gttgtccatt 350  
 gaactgggaa tatttttcaat ccagctgcta cttcttttct actgacacca 400  
 tttctctgggc gttaagttta aagaactgct cagccatggg ggctcacctg 450  
 gtgggttatca actcacagga ggagcaggaa ttcctttcct acaagaaacc 500  
 taaaatgaga gagtttttta ttggactgtc agaccagggt gtcgagggtc 550  
 agtggcaatg ggtggacggc acacctttga caaagtctct gagcttcttg 600  
 gatgtagggg agcccaacaa catagctacc ctggaggact gtgccaccat 650  
 gagagactct tcaaacccaa ggcaaaattg gaatgatgta acctgtttcc 700  
 tcaattattt tcggatttgt gaaatggtag gaataaatcc tttgaacaaa 750



ggaaaatctc tttaagaaca gaaggcacia ctcaaagtgt taaagaagga 800  
 agagcaagaa catggccaca cccaccgccc cacacgagaa atttgtgcgc 850  
 tgaacttcaa aggacttcat aagtatttgt tactctgata caaataaaaa 900  
 taagtagttt taaatgttaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 950  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa 997

<210> 377

<211> 219

<212> PRT

<213> Homo Sapien

<400> 377

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				20					25						
Ile	Leu	Phe	Leu	Ser	Ala	Cys	Phe	Ile	Thr	Arg	Cys	Val	Val	Thr	45
				35					40						
Phe	Arg	Ile	Phe	Gln	Thr	Cys	Asp	Glu	Lys	Lys	Phe	Gln	Leu	Pro	60
				50					55						
Glu	Asn	Phe	Thr	Glu	Leu	Ser	Cys	Tyr	Asn	Tyr	Gly	Ser	Gly	Ser	75
				65					70						
Val	Lys	Asn	Cys	Cys	Pro	Leu	Asn	Trp	Glu	Tyr	Phe	Gln	Ser	Ser	90
				80					85						
Cys	Tyr	Phe	Phe	Ser	Thr	Asp	Thr	Ile	Ser	Trp	Ala	Leu	Ser	Leu	105
				95					100						
Lys	Asn	Cys	Ser	Ala	Met	Gly	Ala	His	Leu	Val	Val	Ile	Asn	Ser	120
				110					115						
Gln	Glu	Glu	Gln	Glu	Phe	Leu	Ser	Tyr	Lys	Lys	Pro	Lys	Met	Arg	135
				125					130						
Glu	Phe	Phe	Ile	Gly	Leu	Ser	Asp	Gln	Val	Val	Glu	Gly	Gln	Trp	150
				140					145						
Gln	Trp	Val	Asp	Gly	Thr	Pro	Leu	Thr	Lys	Ser	Leu	Ser	Phe	Trp	165
				155					160						
Asp	Val	Gly	Glu	Pro	Asn	Asn	Ile	Ala	Thr	Leu	Glu	Asp	Cys	Ala	180
				170					175						

Thr Met Arg Asp Ser Ser Asn Pro Arg Gln Asn Trp Asn Asp Val  
                                   185                                  190                                  195

Thr Cys Phe Leu Asn Tyr Phe Arg Ile Cys Glu Met Val Gly Ile  
                                   200                                  205                                  210

Asn Pro Leu Asn Lys Gly Lys Ser Leu  
                                   215

<210> 378

<211> 21

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<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 378

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<210> 379

<211> 24

<212> DNA

<213> Artificial Sequence

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<223> Synthetic Oligonucleotide Probe

<400> 379

tattcctacc atttcacaaa tccg 24

<210> 380

<211> 49

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 380

ggaggactgt gccaccatga gagactcttc aaaccaagg caaaattgg 49

<210> 381

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 381

gcagattttg aggacagcca cctcca 26

<210> 382  
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<220>  
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<400> 382  
ggccttgcag acaaccgt 18

<210> 383  
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<223> Synthetic oligonucleotide probe

<400> 383  
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<220>  
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<400> 384  
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<210> 385  
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<400> 386

cacaaactcg aactgcttct g 21

<210> 387

<211> 18

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<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 387

gggccatcac agctccct 18

<210> 388

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 388

gggatgtggt gaacacagaa ca 22

<210> 389

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 389

tgccagctgc atgctgccag tt 22

<210> 390

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 390

cagaaggatg tcccgtggaa 20

<210> 391

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 391  
gacgctgtcc actgcag 17

<210> 392  
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<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 392  
gacggcatcc tcagggccac a 21

<210> 393  
<211> 20  
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<213> Artificial Sequence

<220>  
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<400> 393  
atgtcctcca tgcccacgcg 20

<210> 394  
<211> 20  
<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 394  
gagtgcgaca tcgagagctt 20

<210> 395  
<211> 18  
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<220>  
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<400> 395  
ccgcagcctc agtgatga 18

<210> 396  
<211> 21  
<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 396  
gaagagcaca gctgcagatc c 21

<210> 397  
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<220>  
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<400> 397  
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<210> 398  
<211> 20  
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<220>  
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<400> 398  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 399  
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<210> 400  
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<400> 400  
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<210> 401  
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<212> DNA  
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<220>  
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<400> 401  
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<210> 402  
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<400> 402  
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<210> 403  
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<400> 403  
gccaagggtg gtgttagata gg 22

<210> 404  
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<400> 404  
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<210> 405  
<211> 23  
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<220>  
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<400> 405  
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<210> 406  
<211> 26  
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<223> Synthetic oligonucleotide probe  
  
<400> 406  
caggettaca atgttatgat cagaca 26  
  
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<210> 408  
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<400> 408  
tctacatcag cctctctgcg c 21  
  
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<210> 410  
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<210> 411

<211> 23

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 411

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<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 412

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<210> 413

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 413

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<210> 414

<211> 21

<212> DNA

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<400> 414

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<210> 415

<211> 22

<212> DNA

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<400> 415

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<210> 416

<211> 21

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 416

tcaacccctg accctttcct a 21

<210> 417

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 417

ggcaggggac aagccatctc tcct 24

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<213> Artificial Sequence

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<400> 418

gggactgaac tgccagcttc 20

<210> 419

<211> 22

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 419

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<210> 420

<211> 23

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 420

tgtctgcctc agccccagga agg 23

<210> 421

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 421

tctgtccacc atcttgccctt g 21

<210> 422

<211> 3554

<212> DNA

<213> Homo Sapien

<400> 422

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 cttcttctctg ctgctgcttt tcaggggctg cctgataggg gctgtaaatc 150  
 tcaaattccag caatcgaacc ccagtggtag aggaatttga aagtgtggaa 200  
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 gaagaaaatt caagatgaac aaaccacata tgtgtttttt gacaacaaaa 300  
 ttcagggaga cttggcgggg cgtgcagaaa tactggggaa gacatccctg 350  
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 cgttgctcga aatgaccgca aggaaattga tgagatttg atcgagttaa 450  
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 ccagtaggca agatggcaac actgcactgc caggagagtg agggccaccc 550  
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<211> 310

<212> PRT

<213> Homo Sapien

<400> 423

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Ala	Val	Asn	Leu	Lys	Ser	Ser	Asn	Arg	Thr	Pro	Val	Val	Gln	Glu	35	40	45	
Phe	Glu	Ser	Val	Glu	Leu	Ser	Cys	Ile	Ile	Thr	Asp	Ser	Gln	Thr	50	55	60	
Ser	Asp	Pro	Arg	Ile	Glu	Trp	Lys	Lys	Ile	Gln	Asp	Glu	Gln	Thr	65	70	75	
Thr	Tyr	Val	Phe	Phe	Asp	Asn	Lys	Ile	Gln	Gly	Asp	Leu	Ala	Gly	80	85	90	
Arg	Ala	Glu	Ile	Leu	Gly	Lys	Thr	Ser	Leu	Lys	Ile	Trp	Asn	Val	95	100	105	
Thr	Arg	Arg	Asp	Ser	Ala	Leu	Tyr	Arg	Cys	Glu	Val	Val	Ala	Arg	110	115	120	
Asn	Asp	Arg	Lys	Glu	Ile	Asp	Glu	Ile	Val	Ile	Glu	Leu	Thr	Val	125	130	135	
Gln	Val	Lys	Pro	Val	Thr	Pro	Val	Cys	Arg	Val	Pro	Lys	Ala	Val	140	145	150	
Pro	Val	Gly	Lys	Met	Ala	Thr	Leu	His	Cys	Gln	Glu	Ser	Glu	Gly	155	160	165	
His	Pro	Arg	Pro	His	Tyr	Ser	Trp	Tyr	Arg	Asn	Asp	Val	Pro	Leu	170	175	180	
Pro	Thr	Asp	Ser	Arg	Ala	Asn	Pro	Arg	Phe	Arg	Asn	Ser	Ser	Phe	185	190	195	

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Lys	Asp	Asp	Ser	Gly	Gln	Tyr	Tyr	Cys	Ile	Ala	Ser	Asn	Asp	Ala
				215					220					225
Gly	Ser	Ala	Arg	Cys	Glu	Glu	Gln	Glu	Met	Glu	Val	Tyr	Asp	Leu
				230					235					240
Asn	Ile	Gly	Gly	Ile	Ile	Gly	Gly	Val	Leu	Val	Val	Leu	Ala	Val
				245					250					255
Leu	Ala	Leu	Ile	Thr	Leu	Gly	Ile	Cys	Cys	Ala	Tyr	Arg	Arg	Gly
				260					265					270
Tyr	Phe	Ile	Asn	Asn	Lys	Gln	Asp	Gly	Glu	Ser	Tyr	Lys	Asn	Pro
				275					280					285
Gly	Lys	Pro	Asp	Gly	Val	Asn	Tyr	Ile	Arg	Thr	Asp	Glu	Glu	Gly
				290					295					300
Asp	Phe	Arg	His	Lys	Ser	Ser	Phe	Val	Ile					
				305					310					